



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 165030

**TO: Louis V Wollenberger**  
**Location: REM-3B61#2C18**  
**Art Unit: 1635**  
**Thursday, September 15, 2005**

**Case Serial Number: 10/721693**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**Remsen 1-A-62**  
**Phone: 571-272-2524**

**maryjane.ruhl@uspto.gov**

### Search Notes

Examiner Wollenberger,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524



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165030

From: Wollenberger, Louis V.  
Sent: Wednesday, September 07, 2005 2:32 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request

September 7, 2005

Re: Patent Application No. 10/721,693

CRFE

Please carry out the following sequence searches for the above identified application:

1. A length limited search of oligonucleotide SEQ ID NO:1, where the lower limit is 15 and the upper limit is 30.
2. A length limited search of oligonucleotide SEQ ID NO:2, where the lower limit is 15 and the upper limit is 30.

Thanks,  
Louis Wollenberger  
Examiner, Art Unit 1635  
REM-3B-61, Mailbox 2C-18  
x2-8144

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 16:58:36 ; Search time 278.5 Seconds  
(without alignments)  
495.196 Million cell updates/sec

Title: US-10-721-693-2

Perfect score: 21

Sequence: 1 aattcgttgcctcgtcttgg 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7001036

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
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21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	19	US-10-721-693-2
2	21	100.0	21	19	US-10-721-693-4
3	21	100.0	21	20	US-10-852-997-2
4	21	100.0	21	20	US-10-852-997-4
5	19	90.5	21	19	US-10-721-693-1
6	19	90.5	21	19	US-10-721-693-3
7	19	90.5	21	20	US-10-852-997-1

c	8	19	90.5	21	20	US-10-852-997-3	Sequence 3, Appli
c	9	13	61.9	25	21	US-10-719-900-569157	Sequence 569157,
c	10	12	57.1	25	21	US-10-719-900-49468	Sequence 49468, A
c	11	12	57.1	25	21	US-10-719-900-272193	Sequence 272193,
c	12	12	57.1	25	21	US-10-719-900-399511	Sequence 399511,
c	13	12	57.1	25	21	US-10-719-900-911843	Sequence 911843,
c	14	12	57.1	25	21	US-10-719-900-911844	Sequence 911844,
c	15	12	57.1	25	21	US-10-719-900-950357	Sequence 950357,
c	16	12	57.1	25	21	US-10-956-157-278869	Sequence 278869,
c	17	12	57.1	25	22	US-10-719-956-202563	Sequence 202563,
c	18	12	57.1	25	22	US-10-719-956-435371	Sequence 425371,
c	19	12	57.1	25	22	US-10-719-956-573056	Sequence 573056,
c	20	12	57.1	30	14	US-10-014-670-2	Sequence 2, Appli
c	21	12	57.1	30	19	US-10-450-380-2	Sequence 31, Appli
c	22	11	52.4	20	15	US-10-244-367-31	Sequence 143, App
c	23	11	52.4	20	16	US-10-109-349A-143	Sequence 202, App
c	24	11	52.4	20	17	US-10-448-836-202	Sequence 202, App
c	25	11	52.4	20	17	US-10-448-914A-202	Sequence 202, App
c	26	11	52.4	21	20	US-10-751-736-14580	Sequence 14580, A
c	27	11	52.4	21	20	US-10-751-736-19971	Sequence 19971, A
c	28	11	52.4	21	20	US-10-751-736-20001	Sequence 20001, A
c	29	11	52.4	21	20	US-10-751-736-46366	Sequence 46366, A
c	30	11	52.4	21	20	US-10-751-736-46367	Sequence 46367, A
c	31	11	52.4	22	21	US-10-933-611-11	Sequence 11, Appli
c	32	11	52.4	22	21	US-10-933-611-12	Sequence 15, Appli
c	33	11	52.4	22	21	US-10-933-611-15	Sequence 16, Appli
c	34	11	52.4	22	21	US-10-933-611-16	Sequence 61106, A
c	35	11	52.4	25	21	US-10-719-900-61106	Sequence 142642,
c	36	11	52.4	25	21	US-10-719-900-142642	Sequence 206389,
c	37	11	52.4	25	21	US-10-719-900-206389	Sequence 206837,
c	38	11	52.4	25	21	US-10-719-900-206837	Sequence 248436,
c	39	11	52.4	25	21	US-10-719-900-248436	Sequence 256115,
c	40	11	52.4	25	21	US-10-719-900-256115	Sequence 290010,
c	41	11	52.4	25	21	US-10-719-900-290010	Sequence 297061,
c	42	11	52.4	25	21	US-10-719-900-297061	Sequence 297062,
c	43	11	52.4	25	21	US-10-719-900-297062	Sequence 363988,
c	44	11	52.4	25	21	US-10-719-900-363988	Sequence 369589,
c	45	11	52.4	25	21	US-10-719-900-369589	

ALIGNMENTS

RESULT 1  
US-10-721-693-2  
; Sequence 2, Application US/10721693  
; Publication No. US20040162255A1  
; GENERAL INFORMATION:  
; APPLICANT: Medtronic, Inc.  
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv  
; TITLE OF INVENTION: siRNA  
; FILE REFERENCE: P11089.00  
; CURRENT APPLICATION NUMBER: US/10/721,693  
; CURRENT FILING DATE: 2003-11-25  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-721-693-2

Query Match 100.0%; Score 21; DB 19; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCTGTCCTCGCTCTTGG 21  
|||||  
Db 1 AATTCTGTCCTCGCTCTTGG 21

RESULT 2

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US-10-721-693-4
; Sequence 4, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-4

Query Match      100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
Db 1 AATTCGTTGCTCCGCTCTTGG 21

RESULT 3
US-10-852-997-2
; Sequence 2, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-2

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Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
Db 1 AATTCGTTGCTCCGCTCTTGG 21

RESULT 4
US-10-852-997-4
; Sequence 4, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
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; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-4

Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
Db 1 AATTCGTTGCTCCGCTCTTGG 21

RESULT 5
US-10-721-693-1/c
; Sequence 1, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-1

Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCGTTGCTCCGCTCTTGG 21
Db 21 TTCGTTGCTCCGCTCTTGG 3

RESULT 6
US-10-721-693-3/c
; Sequence 3, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-3

Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCGTTGCTCCGCTCTTGG 21
Db 21 TTCGTTGCTCCGCTCTTGG 3
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Db      21  TTGCTGCTCCGCTCTGG 3
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RESULT 7
US-10-852-997-1/c
; Sequence 1, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-1

Query Match      90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  TTGCTGCTCCGCTCTGG 21
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Db      21  TTGCTGCTCCGCTCTGG 3
      |||||||
RESULT 8
US-10-852-997-3/c
; Sequence 3, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-3

Query Match      90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  TTGCTGCTCCGCTCTGG 21
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Db      21  TTGCTGCTCCGCTCTGG 3
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RESULT 9
US-10-719-900-569157
; Sequence 569157, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 569157
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-569157

Query Match      61.9%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AATTCGTTGCTCC 13
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Db      5  AATTCGTTGCTCC 17
      |||||||
RESULT 10
US-10-719-900-49468/c
; Sequence 49468, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-49468

Query Match      57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7  TTGCTCCGCTCT 18
      |||||||
Db      21  TTGCTCCGCTCT 10
      |||||||
RESULT 11
US-10-719-900-272193
; Sequence 272193, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 272193
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-272193

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Query Match 57.1%; Score 12; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TGCTCGCTCTT 19  
Db 4 TGCTCGCTCTT 15

RESULT 12  
US-10-719-900-399511/c  
; Sequence 399511, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 399511  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-399511

Query Match 57.1%; Score 12; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGGCTCTTGG 21  
Db 23 CTCGGCTCTTGG 12

RESULT 13  
US-10-719-900-911843  
; Sequence 911843, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 911843  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-911843

Query Match 57.1%; Score 12; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCGCTCTT 18  
Db 14 TTGCTCGCTCTT 25

RESULT 14  
US-10-719-900-911844  
; Sequence 911844, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 911844  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-911844

Query Match 57.1%; Score 12; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCGCTCTT 18  
Db 14 TTGCTCGCTCTT 25

RESULT 15  
US-10-719-900-950357/c  
; Sequence 950357, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 950357  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-950357

Query Match 57.1%; Score 12; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TGCTCGCTCTT 19  
Db 24 TGCTCGCTCTT 13

Search completed: September 12, 2005, 18:20:28  
Job time : 279.5 secs



```

/clone_lib="lib19 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu'. Grid AA was grown at UC San Diego in 2002.
was extracted from leaf strips, double digested using

```

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 47.6%; Score 10; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTCCGCTCT 18  
 |||  
 Db 20 GCTCCGCTCT 11

## RESULT 2

R60473 28 bp mRNA linear EST 24-MAY-1995  
 LOCUS Yh13g06.r1 Soares infant brain IN1B Homo sapiens cDNA clone  
 DEFINITION IMAGE:43057 5' similar to SP:SYNP\_RAT P22831 ; mRNA sequence.

ACCESSION R60473 GI:831168  
 VERSION EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 28)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.

## TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: M13RP1

High quality sequence stop: 1.

## FEATURES

## source

1. .28  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:415598"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:43057"  
 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares infant brain IN1B"  
 /notes="Organ: whole brain; Vector: Lnfmid BA; Site:1: Not  
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
 I - oligo(dT) primer 15'  
 AACTGAGAATTCCGGCCGAGGAATTTTTTTTTTTT 3'];  
 double-stranded cDNA was ligated to Hind III adaptors  
 (Pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the Lnfmid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 47.6%; Score 10; DB 7; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCCGCT 16  
 |||  
 Db 15 TTGCTCCGCT 24

## RESULT 3

AZ599480/c 19 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0414C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0414C20 R, genomic survey sequence.

ACCESSION AZ599480

VERSION GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0414 row: C column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

## source

1. .19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0414C20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: FWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (G14732114|9b|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCTCCGCTC 17  
|||||

Db 16 GCTCCGCTC 8

RESULT 4  
AJ593450  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
380F06, genomic survey sequence.

ACCESSION  
AJ593450  
VERSION  
AJ593450.1 GI:37943074  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1  
Auteurs  
Brunaud V., Balzerque S., Dubreucq B., Aubourg S., Samson F.,  
Chauvin S., Bechtold N., Cruaud C., DeRose R., Pelletier G.,  
Lepiniec L., Caboche M. and Lecharny A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
JOURNAL  
MEDLINE  
PUBMED  
22363535  
12445656

REFERENCE  
2 (bases 1 to 20)  
Auteurs  
Balzerque S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).

FEATURES  
source  
1..20  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Waslillewska"j  
/db\_xref="taxon:3702"  
/clone="380F06"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1..20  
/notes="T-DNA flanking sequence  
left border"

ORIGIN  
Query Match 42.9%; Score 9; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCTTGCTC 12  
|||||

Db 2 TCCTTGCTC 10

RESULT 5  
BH905710  
LOCUS  
DEFINITION  
SALK\_107640.42.05.x Arabidopsis thaliana T-DNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_107640.42.05.x, genomic  
survey sequence.

ACCESSION  
BH905710  
VERSION  
BH905710.1 GI:22718643  
KEYWORDS  
GSS.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1 (bases 1 to 22)  
Auteurs  
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R.,  
Gadrinab C., Jeske A., Karnes M., Kim C.J., Parker H., Prednis L.,  
Shinn P., Zimmerman J. and Ecker J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
COMMENT  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
T-DNA. This sequence lies within 300 bases of the 5' end of  
At3g33595.  
Class: T-DNA tagged.

FEATURES  
Location/Qualifiers  
source  
1..22  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_107640.42.05.x"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more T-DNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN  
Query Match 42.9%; Score 9; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCGTTG 9  
|||||

Db 10 AATTCGTTG 18  
|||||

RESULT 6  
AJ597633  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
454D02, genomic survey sequence.

ACCESSION  
AJ597633  
VERSION  
AJ597633.1 GI:37947261  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1  
Auteurs  
Brunaud V., Balzerque S., Dubreucq B., Aubourg S., Samson F.,  
Chauvin S., Bechtold N., Cruaud C., DeRose R., Pelletier G.,  
Lepiniec L., Caboche M. and Lecharny A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
JOURNAL  
MEDLINE  
PUBMED  
22363535  
12445656

```

REFERENCE
AUTHORS      2 (bases 1 to 24)
TITLE        Direct Submission
JOURNAL      Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
COMMENT      Gaston Cremieux, 91057 Evry cedex, FRANCE
              PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infoibio.gen.fr).

FEATURES
    source
        1..24
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassiliewskaja"
            /db_xref="taxon:3702"
            /clone="454D02"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    misc_feature
        1..24
            /note="T-DNA flanking sequence
            left border"

ORIGIN
Query Match      42.9%; Score 9; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AATTCGTTG 9
        |||||
Db      16 AATTCGTTG 24

RESULT 7
BM399181/c
LOCUS      5009-0-54-F03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION      Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399181
VERSION        BM399181.1 GI:18199234
KEYWORDS       EST.
SOURCE         Tetrahymena thermophila
ORGANISM       Tetrahymena thermophila
               Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
               Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE
AUTHORS       Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
               Frankel, J. and Klobutcher, L.
TITLE         EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL       Unpublished (2002)
COMMENT       Contact: Turkewitz AP
               Molecular Genetics and Cell Biology
               University of Chicago
               920 E. 58th Street, Chicago, IL 60637, USA
               Tel: 773 702 4374
               Fax: 773 702 3172
               Email: apturkew@midway.uchicago.edu
               Seq primer: T3.
               Location/Qualifiers
                   1..25
                       /organism="Tetrahymena thermophila"
                       /mol_type="mRNA"
                       /strain="CU428.1"
                       /db_xref="taxon:5911"
                       /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                       /notes="Vector: Bluescript2 SK+; Details on library
                       preparation can be found in Chilcoat and Turkewitz (2001)
                       Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
    source
        1..25
            /organism="Tetrahymena thermophila"
            /mol_type="mRNA"
            /strain="CU428.1"
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /notes="Vector: Bluescript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."

```

```

ORIGIN
Query Match      42.9%; Score 9; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 GCTCCGCTC 17
        |||||
Db      9 GCTCCGCTC 1

RESULT 8
AZ861916/c
LOCUS      2M0168K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC2M0168K17 R, genomic survey sequence.
ACCESSION      AZ861916
VERSION        AZ861916.1 GI:13058714
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
               Niederhausern, A. and Wright, D., Weiss, R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: dunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0168 row: K column: 17
               Seq primer: CACACAGAAACAGTATGACC
               Class: plasmid ends
               High quality sequence stop: 30.
               Location/Qualifiers
                   1..30
                       /organism="Mus musculus"
                       /mol_type="genomic DNA"
                       /strain="C57BL/6J"
                       /db_xref="taxon:10090"
                       /clone="UUGC2M0168K17"
                       /sex="Male"
                       /lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                       /notes="Vector: PWD42nv; Purified genomic DNA from M.
                       musculus C57BL/6J (male) was obtained from the Jackson
                       Laboratory Mouse DNA Resource
                       (http://www.jax.org/resources/documents/dnares/). The DNA
                       was hydrodynamically sheared by repeated passage through a
                       0.005 inch orifice at constant velocity. The sheared DNA
                       was blunt end-repaired with T4 DNA polymerase and T4
                       polynucleotide kinase. Adaptor oligonucleotides were
                       ligated to the blunt ends in high molar excess. The
                       adaptor DNA was purified and size-selected for a 9.5 to
                       10.5 kb range using preparative agarose gel
                       electrophoresis. Vector DNA was prepared from a derivative
                       of PWD42 (G14732114|cb|AF129072.1), a copy-number
                       inducible derivative of plasmid R1. The vector was ligated
                       with adaptors complementary to the insert adaptors and
                       purified. The sheared, adaptor mouse DNA was annealed to
                       adapted vector DNA, and transformed into
                       chemically-competent E. coli XL10-Gold (Stratagene) cells
                       and selected for ampicillin resistance."

```

## ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTCCGCTC 17  
|||||  
Db 17 GCTCCGCTC 9

## RESULT 9

BH906565/c

## LOCUS

DEFINITION SALK\_033965.21.05.x Arabidopsis thaliana DNA linear GSS 04-SEP-2002  
Arabidopsis thaliana genomic clone SALK\_033965.21.05.x, genomic survey sequence.

## ACCESSION

BH906565

## VERSION

BH906565.1

## KEYWORDS

GSS.

## SOURCE

Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

## REFERENCE

1 (bases 1 to 30)

## AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

## TITLE

A Sequence-Indexed Library of Insertion Mutations in the

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.

Class: TDNA tagged.

## FEATURES

source

Location/Qualifiers

1..30  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="SALK\_033965.21.05.x"  
/note="PCR was performed on Arabidopsis thaliana DNA insertion lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTG 9  
|||||  
Db 28 AATTCGTTG 20

## RESULT 10

BZ765015/c

## LOCUS

DEFINITION SALK\_127827.19.55.x Arabidopsis thaliana DNA linear GSS 13-MAR-2003  
Arabidopsis thaliana genomic clone SALK\_127827.19.55.x, genomic survey sequence.

## ACCESSION

BZ765015

## VERSION

BZ765015.1

## KEYWORDS

GSS.

## SOURCE

Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

## REFERENCE

1 (bases 1 to 30)

## AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

## TITLE

A Sequence-Indexed Library of Insertion Mutations in the

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.

Class: TDNA tagged.

## FEATURES

source

Location/Qualifiers

1..30  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_127827.19.55.x"  
/note="PCR was performed on Arabidopsis thaliana DNA insertion lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTG 9  
|||||  
Db 30 AATTCGTTG 22

## RESULT 11

BM398577/c

## LOCUS

DEFINITION 5009-0-47-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

## ACCESSION

BM398577

## VERSION

BM398577.1

## KEYWORDS

EST.

## SOURCE

Tetrahymena thermophila

## ORGANISM

Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

## REFERENCE

1 (bases 1 to 18)

## AUTHORS

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172

```

Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCTCCGCT 16
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RESULT 12
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LOCUS
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    7LEAF--03-D20.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
    sativa (japonica cultivar-group) cDNA clone 7LEAF--03-D20, mRNA
    sequence.
ACCESSION
    CF299279
VERSION
    CF299279.1 GI:33671040
KEYWORDS
    EST.
SOURCE
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    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
    1 (bases 1 to 19)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATTCGTT 8
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Db 12 AATTCGTT 5

Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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        5009-0-34-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
        Tetrahymena thermophila cDNA, mRNA sequence.
        BM397580
        BM397580.1 GI:18197633
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        Tetrahymena thermophila
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        Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
        Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
        1 (bases 1 to 20)
        Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
        Frankel,J. and Klobutcher,L.
        EST from Tetrahymena thermophila, strain CU428.1, growing cells
        Unpublished (2002)
        Contact: Turkewitz AP
        Molecular Genetics and Cell Biology
        University of Chicago
        920 E. 58th Street, Chicago, IL 60637, USA
        Tel: 773 702 4374
        Fax: 773 702 3172
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                Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Db 9 GCTCCGCT 2

RESULT 14
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LOCUS
DEFINITION
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ACCESSION
    BM398685
VERSION
    BM398685.1 GI:18198738
KEYWORDS
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SOURCE
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    Tetrahymena thermophila
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    Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
    1 (bases 1 to 20)
    Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
    Frankel,J. and Klobutcher,L.
    EST from Tetrahymena thermophila, strain CU428.1, growing cells
    Unpublished (2002)
    Contact: Turkewitz AP
    Molecular Genetics and Cell Biology
    University of Chicago
    920 E. 58th Street, Chicago, IL 60637, USA
    Tel: 773 702 4374
    Fax: 773 702 3172
    Email: apturkew@midway.uchicago.edu
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCTCCGCT 16
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DEFINITION      5009-0-S1-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM398964
VERSION      BM398964.1 GI:18199017
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 20)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Best Local Similarity 100.0%; Pred. No. 1.9e+06;
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Db      9 GCTCCGCT 2

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop\_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

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Total number of hits satisfying chosen parameters: 1308090

Minimum DB seq length: 15  
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

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- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	CQ824574
2	21	100.0	21	6	CQ824576
3	19	90.5	21	6	CQ824575
4	19	90.5	21	6	CQ824577
5	11	52.4	20	6	E30575
6	11	52.4	20	6	AR268863
7	11	52.4	20	6	AR442594
8	11	52.4	22	6	AR568156
9	11	52.4	25	6	AX469952
10	11	52.4	29	6	AR031175
11	11	52.4	30	6	AR098219
12	11	52.4	30	6	BD195066
13	10	47.6	16	6	AR328457
14	10	47.6	17	6	AR243693
15	10	47.6	17	6	AR327452
16	10	47.6	17	6	AR327453
17	10	47.6	17	6	AX736243
18	10	47.6	18	6	AX229718
19	10	47.6	18	6	AX402871

C 20	10	47.6	18	6	AX497756	Sequence 18
C 21	10	47.6	18	6	AX822220	Sequence 18
C 22	10	47.6	18	6	AX825860	Sequence 18
C 23	10	47.6	19	6	AR233719	Sequence 19
C 24	10	47.6	20	6	AS1886	Sequence 20
C 25	10	47.6	20	6	AS2459	Sequence 20
C 26	10	47.6	20	6	AR7520	Sequence 20
C 27	10	47.6	20	6	AR085851	Sequence 20
C 28	10	47.6	20	6	AR111715	Sequence 20
C 29	10	47.6	20	6	CQ784255	Sequence 20
C 30	10	47.6	20	6	AR299168	Sequence 20
C 31	10	47.6	20	6	AR314772	Sequence 20
C 32	10	47.6	20	6	AR314991	Sequence 20
C 33	10	47.6	20	6	AR315108	Sequence 20
C 34	10	47.6	20	6	AR315109	Sequence 20
C 35	10	47.6	20	6	AR337038	Sequence 20
C 36	10	47.6	20	6	AX296790	Sequence 20
C 37	10	47.6	20	6	AX298426	Sequence 20
C 38	10	47.6	20	6	AX743209	Sequence 20
C 39	10	47.6	20	6	AX956649	Sequence 20
C 40	10	47.6	20	6	BD128179	Primer 20
C 41	10	47.6	21	6	AR164118	Sequence 21
C 42	10	47.6	21	6	CQ786389	Sequence 21
C 43	10	47.6	21	6	AX363185	Sequence 21
C 44	10	47.6	22	6	A48928	Sequence 22
C 45	10	47.6	22	6	AR153363	Sequence 22

ALIGNMENTS

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LOCUS	CQ824574					
DEFINITION	CQ824574					
ACCESSION	CQ824574					
VERSION	CQ824574.1	GI:49021592				
KEYWORDS						
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REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
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DEFINITION	CQ824576			
ACCESSION	CQ824576			
VERSION	CQ824576.1	GI:49021596		
KEYWORDS				
SOURCE				
ORGANISM				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1  
REFERENCE  
AUTHORS Kaemerer, W.F.  
TITLE Treatment of neurodegenerative disease through intracranial  
delivery of siRNA  
JOURNAL Patent: WO 2004047872-A 3 10-JUN-2004;  
Medtronic, Inc. (US)  
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ACCESSION CQ824575  
VERSION CQ824575.1 GI:49021594  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1  
REFERENCE  
AUTHORS Kaemerer, W.F.  
TITLE Treatment of neurodegenerative disease through intracranial  
delivery of siRNA  
JOURNAL Patent: WO 2004047872-A 2 10-JUN-2004;  
Medtronic, Inc. (US)  
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LOCUS CQ824577 21 bp DNA linear PAT 21-JUN-2004  
DEFINITION Sequence 4 from Patent WO2004047872.  
ACCESSION CQ824577  
VERSION CQ824577.1 GI:49021598  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1  
REFERENCE  
AUTHORS Kaemerer, W.F.  
TITLE Treatment of neurodegenerative disease through intracranial  
delivery of siRNA  
JOURNAL Patent: WO 2004047872-A 4 10-JUN-2004;

Medtronic, Inc. (US)  
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Db 21 CCAAGAGCGGAGCAACGAA 3  
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DEFINITION Neurogenesis-inductive gene.  
ACCESSION E30575  
VERSION E30575.1 GI:13017145  
KEYWORDS JP 199341985-A/28.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Katsuhiko, M., Jun, A., Kenji, N. and Katsunori, N.  
TITLE Neurogenesis-inductive gene  
JOURNAL Patent: JP 199341985-A 28 14-DEC-1999;  
RIKAGAKU KENKYUSHO  
OS Unidentified  
PN JP 199341985-A/28  
PD 14-DEC-1999  
PP 30-APR-1998 JP 1998121456  
PR KATSUHIKO MIKOSHIBA, JUN ARIGA, KENJI NAGAI, KATSUNORI NAKATA PC  
C12N15/09, A61K35/74, A61K38/76, A61K38/00, A61K48/00, PC  
C07K14/47,  
PC C12N1/21, C12N5/10, C12P21/02, C12R1/91, C12R1/91), (C12N1/21,  
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PC C12N15/00,  
PC A61K37/02, A61K37/02, C12N5/00, (C12N15/00, C12R1/91), (C12N5/00,  
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DEFINITION Sequence 31 from patent US 650637.  
ACCESSION AR268863  
VERSION AR268863.1 GI:29699559

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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 20)
AUTHORS       Mikoshiba,K., Aruga,J., Nagai,T. and Nakata,K.
TITLE         Neurogenesis inducing genes
JOURNAL       Patent: US 650637-A 31 31-DEC-2002;
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QY 4 CAAGAGCGGAG 14
Db 1 CAAGAGCGGAG 11

RESULT 7
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ACCESSION    AR442594
VERSION      AR442594.1 GI:42669851
KEYWORDS     Unknown.
SOURCE       Unclassified.
ORGANISM     Kim,C.M.; Park,H.K. and Jang,H.J.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Kim,C.M.; Park,H.K. and Jang,H.J.
TITLE        Oligonucleotide for detection and identification of Mycobacteria
JOURNAL      Patent: US 6670130-A 202 30-DEC-2003;
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ACCESSION    AR568156
VERSION      AR568156.1 GI:53986443
KEYWORDS     Unknown.
SOURCE       Unclassified.
ORGANISM     Costa,M.R.; Doberstein,S.K., Elson,S.L., Ferguson,K.C. and
REFERENCE    1 (bases 1 to 22)
AUTHORS      Homburger,S.A.
TITLE        Animal models and methods for analysis of lipid metabolism and
              screening of pharmaceutical and pesticidal agents that modulate
              lipid metabolism
JOURNAL      Patent: US 6781028-A 81 24-AUG-2004;
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RESULT 8
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DEFINITION   Sequence 81 from patent US 6781028.
ACCESSION    AR568156
VERSION      AR568156.1 GI:53986443
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SOURCE       Unclassified.
ORGANISM     Costa,M.R.; Doberstein,S.K., Elson,S.L., Ferguson,K.C. and
REFERENCE    1 (bases 1 to 22)
AUTHORS      Homburger,S.A.
TITLE        Animal models and methods for analysis of lipid metabolism and
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              lipid metabolism
JOURNAL      Patent: US 6781028-A 81 24-AUG-2004;
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QY 11 GGAGCAACGAA 21
Db 22 GGAGCAACGAA 12

RESULT 9
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LOCUS         AX469952
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ACCESSION    AX469952
VERSION      AX469952.1 GI:22205225
KEYWORDS     Escherichia coli
SOURCE       Escherichia coli
ORGANISM     Escherichia coli
REFERENCE    1
AUTHORS      Berghof,K., Grabowski,R., Groenewald,C. and Pardigol,A.
TITLE        Detection of pathogenic bacteria
JOURNAL      Patent: WO 02053771-A 69 11-JUL-2002;
              BIOTECON DIAGNOSTICS GMBH (DE)
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Query Match   52.4%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACCAAGAGCGG 12
Db 23 ACCAAGAGCGG 13

RESULT 10
AR053175
LOCUS         AR053175
DEFINITION   Sequence 81 from patent US 5834183.
ACCESSION    AR053175
VERSION      AR053175.1 GI:5978037
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 29)
AUTHORS      Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE        Gene sequence for spinocerebellar ataxia type 1 and method for
              diagnosis
JOURNAL      Patent: US 5834183-A 81 10-NOV-1998;
FEATURES     Location/Qualifiers
               1..29
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCG 11
Db 19 AACCAAGAGCG 29

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RESULT 11
AR098219 LOCUS AR098219 30 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 42 from patent US 6074851.
ACCESSION AR098219
VERSION AR098219.1 GI:12807476
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Deibel,M.R. Jr., Yem,A.W. and Wolfe,C.L.
TITLE Catalytic macro molecules having cdc25B like activity
JOURNAL Patent: US 6074851-A 42 13-JUN-2000;
FEATURES
    source      Location/Qualifiers
        1..30
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GAGCGGAGCAA 17
Db 4 GAGCGGAGCAA 14

RESULT 12
BD195066 LOCUS BD195066 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Catalytic polymer having CDC25B like activity.
ACCESSION BD195066
VERSION BD195066.1 GI:33004824
KEYWORDS JP 2002515742-A/27.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Jr,M.R.D., Yem,A.W. and Wilson,C.L.
TITLE Catalytic polymer having CDC25B like activity
JOURNAL Patent: JP 2002515742-A 27 28-MAY-2002;
COMMENT PHARMACIA & UPJOHN CO
OS Unidentified
PN JP 2002515742-A/27
PD 28-MAY-2002
PF 02-MAY-1997 JP 1997538892
PR 02-MAY-1996 US 60/016748, 07-MAY-1996 US 60/017323 PI
MARTIN R DEIBEL JR,ANTHONY W YEM,CINDY L WILSON PC
(C12N1/55,C12N15/54,C12N15/62,C12N9/16,C12N9/10,C12N1/21// PC
CC Strandedness: Single;
CC Topology: Linear;
CC Catalytic polymer having CDC25B like activity FH Key
FT Location/Qualifiers
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            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GAGCGGAGCAA 17
Db 4 GAGCGGAGCAA 14

RESULT 13
AR328457 LOCUS AR328457 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5859 from patent US 6566127.
ACCESSION AR328457
VERSION AR328457.1 GI:33714265
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5859 20-MAY-2003;
FEATURES
    source      Location/Qualifiers
        1..16
            /organism="unknown"
            /mol_type="unassigned RNA"
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Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ACCAAGAGCG 11
Db 2 ACCAAGAGCG 11

RESULT 14
AR243693 LOCUS AR243693 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6475996.
ACCESSION AR243693
VERSION AR243693.1 GI:27291128
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cazaux,C., Tiraby,G.J., Fons,P. and Hoffmann,J.-S.
TITLE Use of a vector expressing DNA polymerase .beta. as medicine
JOURNAL Patent: US 6475996-A 5 05-NOV-2002;
FEATURES
    source      Location/Qualifiers
        1..17
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match      47.6%; Score 10; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACCAAGAGC 10
Db 4 ACCCAAGAGC 13

RESULT 15
AR327452 LOCUS AR327452 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4854 from patent US 6566127.
ACCESSION AR327452
VERSION AR327452.1 GI:33713260
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
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related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 4854 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN

Query Match 47.6%; Score 10; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.2e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 ACCAAGAGCG 11  
| | | | | | | |  
Db 7 ACCAAGAGCG 16

Search completed: September 12, 2005, 17:22:23  
Job time : 536.5 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 16:40:43 ; Search time 58 Seconds  
(without alignments)  
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Title: US-10-721-693-2

Perfect score: 21

Sequence: 1 aattcgtgtccgctctgg 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

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Total number of hits satisfying chosen parameters: 914340

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	57.1	22	4	US-09-332-522E-81
2	11	52.4	20	3	US-09-121-520-26
3	11	52.4	20	3	US-09-172-045-31
4	11	52.4	20	4	US-09-342-325C-31
5	11	52.4	20	4	US-09-980-052-202
6	11	52.4	22	5	PCT-US93-12078-2
7	11	52.4	22	5	PCT-US93-12078-3
8	11	52.4	25	4	US-09-396-196G-14051
9	11	52.4	25	4	US-09-396-196G-18109
10	11	52.4	25	4	US-09-396-196G-18110
11	11	52.4	25	4	US-09-396-196G-18111
12	11	52.4	25	4	US-09-396-196G-66426
13	11	52.4	25	4	US-09-396-196G-66427
14	11	52.4	25	4	US-09-396-196G-66438
15	11	52.4	30	3	US-08-848-810-42
16	11	52.4	30	3	US-09-492-985-6
17	10	47.6	18	3	US-09-344-521-22
18	10	47.6	20	3	US-08-875-223-3
19	10	47.6	20	4	US-09-198-452A-5309
20	10	47.6	20	4	US-09-198-452A-5645
21	10	47.6	20	4	US-09-198-452A-5646
22	10	47.6	20	4	US-09-922-146-11
23	10	47.6	20	4	US-10-023-649A-19
24	10	47.6	21	3	US-09-210-896-22
25	10	47.6	22	3	US-08-793-044-7
26	10	47.6	23	3	US-09-102-831-16
27	10	47.6	24	3	US-09-284-900-2

c	28	10	47.6	24	4	US-09-270-767-62514	Sequence 62514, A
c	29	10	47.6	25	1	US-08-379-926A-4	Sequence 4, Appli
c	30	10	47.6	25	3	US-08-866-446-1	Sequence 1, Appli
c	31	10	47.6	25	4	US-09-396-196G-12977	Sequence 12977, A
c	32	10	47.6	25	4	US-09-396-196G-12978	Sequence 12978, A
c	33	10	47.6	25	4	US-09-396-196G-34741	Sequence 34741, A
c	34	10	47.6	25	4	US-09-396-196G-52807	Sequence 52807, A
c	35	10	47.6	25	4	US-09-396-196G-52808	Sequence 52808, A
c	36	10	47.6	25	4	US-09-396-196G-52809	Sequence 52809, A
c	37	10	47.6	25	4	US-09-396-196G-56973	Sequence 56973, A
c	38	10	47.6	25	4	US-09-396-196G-73270	Sequence 73270, A
c	39	10	47.6	25	4	US-09-396-196G-73271	Sequence 73271, A
c	40	10	47.6	25	4	US-09-396-196G-77212	Sequence 77212, A
c	41	10	47.6	25	4	US-09-396-196G-87841	Sequence 87841, A
c	42	10	47.6	25	4	US-09-396-196G-96977	Sequence 96977, A
c	43	10	47.6	25	4	US-09-396-196G-96978	Sequence 96978, A
c	44	10	47.6	25	4	US-09-396-196G-96979	Sequence 96979, A
c	45	10	47.6	25	4	US-09-396-196G-96980	Sequence 96980, A

ALIGNMENTS

RESULT 1  
US-09-332-522E-81  
; Sequence 81, Application US/09332522E  
; Patent No. 6781028  
; GENERAL INFORMATION:  
; APPLICANT: Costa, M.  
; APPLICANT: Doberstein, S.  
; APPLICANT: Elson, S.  
; APPLICANT: Ferguson, K.  
; APPLICANT: Homberger, S.  
; TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND S  
; TITLE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METAB  
; FILE REFERENCE: 7326-101, EX99-004  
; CURRENT APPLICATION NUMBER: US/09/332,522E  
; CURRENT FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 81  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-332-522E-81

Query Match 57.1%; Score 12; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATTCTGTGCTCC 13  
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Db 11 ATTCTGTGCTCC 22

RESULT 2  
US-09-121-920-26/c  
; Sequence 26, Application US/09121920  
; Patent No. 6066460  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Mark W.  
; APPLICANT: Kinoshita, No. 6066460iyuki  
; TITLE OF INVENTION: METHOD FOR CLONING SECRETED PROTEINS  
; FILE REFERENCE: HMV-022.01  
; CURRENT APPLICATION NUMBER: US/09/121,920  
; CURRENT FILING DATE: 1998-07-24  
; EARLIER APPLICATION NUMBER: 60/053,586  
; EARLIER FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 26

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: primer  
; US-09-121-920-26

Query Match 52.4%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGCTCTTG 20  
| | | | | | | | | |  
Db 11 CTCGCTCTTG 1

## RESULT 3

US-09-172-045-31/c  
; Sequence 31, Application US/09172045  
; Patent No. 6277594

; GENERAL INFORMATION:  
; APPLICANT: Mikoshiba, Katsuhiko

; APPLICANT: Aruga, Jun  
; APPLICANT: Nagai, Takeharu

; APPLICANT: Nakata, Katsunori  
; TITLE OF INVENTION: Neurogenesis Inducing Gene

; FILE REFERENCE: Hiraki-03497  
; CURRENT APPLICATION NUMBER: US/09/172,045

; CURRENT FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: JP98/86979

; EARLIER FILING DATE: 1998-03-31  
; EARLIER APPLICATION NUMBER: JP98/121456

; EARLIER FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31

; LENGTH: 20  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-172-045-31

Query Match 52.4%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGCTCTTG 20  
| | | | | | | | | |  
Db 11 CTCGCTCTTG 1

## RESULT 4

US-09-342-325C-31/c

; Sequence 31, Application US/09342325C  
; Patent No. 6500637

; GENERAL INFORMATION:  
; APPLICANT: Mikoshiba, Katsuhiko

; APPLICANT: Aruga, Jun  
; APPLICANT: Nagai, Takeharu

; APPLICANT: Katsunori, Nakata  
; TITLE OF INVENTION: Neurogenesis Inducing Gene

; FILE REFERENCE: HIRAKI-03814  
; CURRENT APPLICATION NUMBER: US/09/342,325C

; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: JP98/86979

; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: JP98/121456

; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 09/172,045

; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31

; LENGTH: 20  
; TYPE: DNA

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-342-325C-31

Query Match 52.4%; Score 11; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGCTCTTG 20  
| | | | | | | | | |  
Db 11 CTCGCTCTTG 1

## RESULT 5

US-09-980-052-202

; Sequence 202, Application US/099800052  
; Patent No. 6670130

; GENERAL INFORMATION:  
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.

; APPLICANT: KIM, Cheol Min  
; APPLICANT: PARK, Hee Kyung

; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria  
; FILE REFERENCE: PP05020/PCT

; CURRENT APPLICATION NUMBER: US/09/980,052  
; CURRENT FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: KR 10-1999-0019631  
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019632  
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019633  
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019634  
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019635  
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-2000-0018189  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 243  
; SOFTWARE: KopatentIn 1.71

; SEQ ID NO 202  
; LENGTH: 20

; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium porcinum  
US-09-980-052-202

Query Match 52.4%; Score 11; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTTGCTCCGCT 16  
| | | | | | | | | |  
Db 10 GTTGCTCCGCT 20

## RESULT 6

PCT-US93-12078-2/c

; Sequence 2, Application PC/TUS9312078  
; GENERAL INFORMATION:

; APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS

; APPLICANT: SYSTEM: 201 West 7th Street

; APPLICANT: STREET: Austin

; APPLICANT: CITY: Texas

; APPLICANT: STATE: United States of America

; APPLICANT: COUNTRY: 78701

; APPLICANT: POSTAL CODE: (512)499-4462

; APPLICANT: TELEPHONE NO: (512)499-4523

; APPLICANT: TELEFAX: POTENT AND SPECIFIC

; TITLE OF INVENTION:



```

; TITLE OF INVENTION: CHEMICALLY-CONJUGATED
; TITLE OF INVENTION: IMMUNOTOXINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12078
; FILING DATE: UNKNOWN
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/992,900
; FILING DATE: 16.12.92
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTFF046PCT
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2676
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-12078-2

Query Match 52.4%; Score 11; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTCGTTGCTC 12
Db 11 ATTCGTTGCTC 1

RESULT 7
PCT-US93-12078-3
; Sequence 3, Application PC/TUS9312078
; GENERAL INFORMATION:
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS
; APPLICANT: NAME:
; APPLICANT: SYSTEM
; APPLICANT: STREET: 201 West 7th Street
; APPLICANT: CITY: Austin
; APPLICANT: STATE: Texas
; APPLICANT: COUNTRY: United States of America
; APPLICANT: POSTAL CODE: 78701
; APPLICANT: TELEPHONE NO: (512)499-4462
; APPLICANT: TELEFAX: (512)499-4523
; TITLE OF INVENTION: POTENT AND SPECIFIC
; TITLE OF INVENTION: CHEMICALLY-CONJUGATED
; TITLE OF INVENTION: IMMUNOTOXINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12078
; FILING DATE: UNKNOWN
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/992,900
; FILING DATE: 16.12.92
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTFF046PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2676
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-12078-3

Query Match 52.4%; Score 11; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTCGTTGCTC 12
Db 12 ATTCGTTGCTC 22

RESULT 8
US-09-396-196G-14051/c
; Sequence 14051, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-14051

Query Match 52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCCGCTCTTGG 21
Db 17 TCCGCTCTTGG 7

RESULT 9
US-09-396-196G-18109
; Sequence 18109, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:

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; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18109

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCGCTCTTGG 21
Db      15 TCCGCTCTTGG 25
|||||

RESULT 10
US-09-396-196G-18110
; Sequence 18110, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18110

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCGCTCTTGG 21
Db      9 TCCGCTCTTGG 19
|||||

RESULT 11
US-09-396-196G-18111
; Sequence 18111, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18110

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCGCTCTTGG 21
Db      24 TTGCTCGCTC 14
|||||

RESULT 12
US-09-396-196G-66426/c
; Sequence 66426, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-66426

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TTGCTCGCTC 17
Db      24 TTGCTCGCTC 14
|||||

RESULT 13
US-09-396-196G-66427/c
; Sequence 66427, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-66427
```

Query Match 52.4%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17  
| | | | | | | | | |  
Db 22 TTGCTCCGCTC 12

RESULT 14  
US-09-396-196G-66438/c  
; Sequence 66438, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 66438  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-66438

Query Match 52.4%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17  
| | | | | | | | | |  
Db 20 TTGCTCCGCTC 10

RESULT 15  
US-08-848-810-42/c  
; Sequence 42, Application US/08848810  
; Patent No. 6074851  
; GENERAL INFORMATION:  
; APPLICANT: Deibel Jr., M. R.  
; APPLICANT: Yem, A. W.  
; APPLICANT: Wilson, C. L.  
; TITLE OF INVENTION: Catalytic Macro Molecules Having DCD25B  
; TITLE OF INVENTION: Like Activity  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Company  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/848,810  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wootton, Thomas A.  
; REGISTRATION NUMBER: 35,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-833-7914

TELEFAX: 616-833-6897  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-848-810-42

Query Match 52.4%; Score 11; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17  
| | | | | | | | | |  
Db 14 TTGCTCCGCTC 4

Search completed: September 12, 2005, 18:11:00  
Job time : 58 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 14:04:18 ; Search time 174 Seconds  
(without alignments)  
714.452 Million cell updates/sec

Title: US-10-721-693-2

Perfect score: 21

Sequence: 1 aattcgtgtcctcgtcttgg 21

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2557800

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

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2: Geneseqn1990s:.\*  
3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002as:.\*  
7: Geneseqn2002bs:.\*  
8: Geneseqn2003as:.\*  
9: Geneseqn2003bs:.\*  
10: Geneseqn2003cs:.\*  
11: Geneseqn2003ds:.\*  
12: Geneseqn2004as:.\*  
13: Geneseqn2004bs:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	12 ADP44614	Adp44614 Antisense
2	21	100.0	21	12 ADP44612	Adp44612 Antisense
C 3	19	90.5	21	12 ADP44613	Adp44613 Sense DNA
C 4	19	90.5	21	12 ADP44611	Adp44611 Sense DNA
C 5	12	57.1	20	2 AAZ03368	Aaz03368 PCR prime
6	12	57.1	30	6 AAL48427	Aal48427 Secreted
C 7	11	52.4	19	12 ADK96972	Adk96972 Primer of
C 8	11	52.4	20	2 AAX19405	Aax19405 Neurogeni
C 9	11	52.4	20	2 AAZ04279	Aaz04279 PCR prime
C 10	11	52.4	20	3 AAZ55953	Aaz55953 Xenopus 1
11	11	52.4	20	4 AAF23328	Aaf23328 Oligonuc
12	11	52.4	20	10 ADD56623	Add56623 Human gen
13	11	52.4	20	10 ABZ97696	Abz97696 Human CCR
14	11	52.4	20	10 ABZ97695	Abz97695 Human CCR
15	11	52.4	20	11 ABD30726	Abd30726 Human CCR
16	11	52.4	20	11 ABD30727	Abd30727 Human CCR
17	11	52.4	20	12 ADJ59552	Adj59552 Oligonuc
18	11	52.4	20	12 ADJ59553	Adj59553 Oligonuc
19	11	52.4	20	12 ADO45043	Ado45043 Human oli
20	11	52.4	20	12 ADO45042	Ado45042 Human oli

C 21	11	52.4	22	2 AAQ68396	Aaq68396 Pseudomon
C 22	11	52.4	29	2 AAX80489	Aax80489 Human sec
C 23	11	52.4	29	4 AAS59324	Aas59324 Human sec
C 24	11	52.4	29	6 ABA90993	Abas90993 Biotinyla
C 25	11	52.4	29	12 ADO61037	Ado61037 Human deb
C 26	11	52.4	30	2 AAQ78253	Aaq78253 Primer to
27	11	52.4	30	3 AAS50463	Aas50463 Human zin
28	10	47.6	17	2 AAV96406	Aav96406 Potato ci
29	10	47.6	17	2 AAV96405	Aav96405 Potato ci
30	10	47.6	17	6 ACN01300	Acn01300 WNV Hamme
C 31	10	47.6	17	6 ACN12384	Acn12384 WNV minus
C 32	10	47.6	17	6 ACN14271	Acn14271 WNV minus
C 33	10	47.6	17	6 ACN04597	Acn04597 WNV Zinzy
C 34	10	47.6	17	6 ACN14270	Acn14270 WNV minus
C 35	10	47.6	17	6 ACN03280	Acn03280 WNV Inozy
36	10	47.6	17	6 ACN04596	Acn04596 WNV Zinzy
C 37	10	47.6	17	6 ACN12383	Acn12383 WNV minus
38	10	47.6	17	6 ACN01301	Acn01301 WNV Hamme
39	10	47.6	17	6 ACN03279	Acn03279 WNV Inozy
C 40	10	47.6	17	6 ACN09757	Acn09757 WNV minus
C 41	10	47.6	17	10 ADI49330	Adi49330 Human tum
42	10	47.6	18	3 AAS52028	Aas52028 Antisense
C 43	10	47.6	18	5 AAS12190	Aas12190 Human Int
44	10	47.6	18	6 AAD40983	Aad40983 Human PI3
C 45	10	47.6	18	6 ABK29394	Abk29394 Penicilli

#### ALIGNMENTS

##### RESULT 1

ADP44614

ID ADP44614 standard; DNA; 21 BP.

AC ADP44614;

DT 26-AUG-2004 (first entry)

DE Antisense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.

XX neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;

KW Huntington's; spinocerebellar ataxia type 1;

KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;

KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;

KW small interfering RNA; ss; human; ataxin 1.

XX Homo sapiens.

OS WO2004047872-A2.

PN 10-JUN-2004.

PD 26-NOV-2003; 2003WO-US037650.

XX 26-NOV-2002; 2002US-0429387P.

PR 03-FEB-2003; 2003US-0444614P.

XX (MEDT ) MEDTRONIC INC.

PA Kaemmerer WF;

XX WPI; 2004-441106/41.

XX New medical system comprising an intracranial access device, a mapping

PT means, a small interfering RNA or vector encoding the RNA, and a delivery

PT means, useful for treating a neurodegenerative disorder.

XX Claim 68; SEQ ID NO 4; 228pp; English.

XX The invention relates to a novel medical system for treating a

CC neurodegenerative disorder comprising an intracranial access device, a

CC mapping means for locating a predetermined location in the brain, a

CC deliverable amount of a small interfering RNA (siRNA), or vector encoding

CC the siRNA, and a delivery means. The system of the invention has  
CC applications related to the CNS and may be useful for treating a  
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
CC The current sequence is that of the antisense DNA 2 encoding an siRNA  
CC targeted to human ataxin 1 mRNA of the invention.  
XX SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 21; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AATTCGTTGCTCCGCTCTTGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AATTCGTTGCTCCGCTCTTGG 21  
  
RESULT 2  
ADP44612  
ID ADP44612 standard; DNA; 21 BP.  
XX  
AC ADP44612;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Antisense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.  
XX  
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;  
KW Huntington's; spinocerebellar ataxia type 1;  
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;  
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;  
KW small interfering RNA; ss; human; ataxin 1.  
XX  
OS Homo sapiens.  
XX  
PN WO2004047872-A2.  
XX  
PD 10-JUN-2004.  
XX  
PF 26-NOV-2003; 2003WO-US037650.  
XX  
PR 26-NOV-2002; 2002US-0429387P.  
PR 03-FEB-2003; 2003US-0444614P.  
XX  
PA (MEDT ) MEDTRONIC INC.  
XX  
PI Kaemmerer WF;  
XX  
DR WPI; 2004-441106/41.  
XX  
PF 26-NOV-2003; 2003WO-US037650.  
XX  
PR 26-NOV-2002; 2002US-0429387P.  
PR 03-FEB-2003; 2003US-0444614P.  
XX  
PA (MEDT ) MEDTRONIC INC.  
XX  
PI Kaemmerer WF;  
XX  
DR WPI; 2004-441106/41.  
XX  
PF New medical system comprising an intracranial access device, a mapping  
PT means, a small interfering RNA or vector encoding the RNA, and a delivery  
PT means, useful for treating a neurodegenerative disorder.  
XX  
PS Claim 68; SEQ ID NO 2; 228pp; English.  
XX  
CC The invention relates to a novel medical system for treating a  
CC neurodegenerative disorder comprising an intracranial access device, a  
CC mapping means for locating a predetermined location in the brain, a  
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding  
CC the siRNA, and a delivery means. The system of the invention has  
CC applications related to the CNS and may be useful for treating a  
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
CC The current sequence is that of the antisense DNA 1 encoding an siRNA  
CC targeted to human ataxin 1 mRNA of the invention.  
XX  
SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 21; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AATTCGTTGCTCCGCTCTTGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AATTCGTTGCTCCGCTCTTGG 21  
  
RESULT 3  
ADP44613/c  
ID ADP44613 standard; DNA; 21 BP.  
XX  
AC ADP44613;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.  
XX  
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;  
KW Huntington's; spinocerebellar ataxia type 1;  
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;  
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;  
KW small interfering RNA; ss; human; ataxin 1.  
XX  
OS Homo sapiens.  
XX  
PN WO2004047872-A2.  
XX  
PD 10-JUN-2004.  
XX  
PF 26-NOV-2003; 2003WO-US037650.  
XX  
PR 26-NOV-2002; 2002US-0429387P.  
PR 03-FEB-2003; 2003US-0444614P.  
XX  
PA (MEDT ) MEDTRONIC INC.  
XX  
PI Kaemmerer WF;  
XX  
DR WPI; 2004-441106/41.  
XX  
PF New medical system comprising an intracranial access device, a mapping  
PT means, a small interfering RNA or vector encoding the RNA, and a delivery  
PT means, useful for treating a neurodegenerative disorder.  
XX  
PS Claim 68; SEQ ID NO 3; 228pp; English.  
XX  
CC The invention relates to a novel medical system for treating a  
CC neurodegenerative disorder comprising an intracranial access device, a  
CC mapping means for locating a predetermined location in the brain, a  
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding  
CC the siRNA, and a delivery means. The system of the invention has  
CC applications related to the CNS and may be useful for treating a  
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
CC The current sequence is that of the sense DNA 2 encoding an siRNA  
CC targeted to human ataxin 1 mRNA of the invention.  
XX  
SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 90.5%; Score 19; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 TTCGTTGCTCCGCTCTTGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 TTCGTTGCTCCGCTCTTGG 3  
  
RESULT 4  
ADP44611/c  
ID ADP44611 standard; DNA; 21 BP.

Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AATTCGTTGCTCCGCTCTTGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AATTCGTTGCTCCGCTCTTGG 21  
  
RESULT 3  
ADP44613/c  
ID ADP44613 standard; DNA; 21 BP.  
XX  
AC ADP44613;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.  
XX  
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;  
KW Huntington's; spinocerebellar ataxia type 1;  
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;  
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;  
KW small interfering RNA; ss; human; ataxin 1.  
XX  
OS Homo sapiens.  
XX  
PN WO2004047872-A2.  
XX  
PD 10-JUN-2004.  
XX  
PF 26-NOV-2003; 2003WO-US037650.  
XX  
PR 26-NOV-2002; 2002US-0429387P.  
PR 03-FEB-2003; 2003US-0444614P.  
XX  
PA (MEDT ) MEDTRONIC INC.  
XX  
PI Kaemmerer WF;  
XX  
DR WPI; 2004-441106/41.  
XX  
PF New medical system comprising an intracranial access device, a mapping  
PT means, a small interfering RNA or vector encoding the RNA, and a delivery  
PT means, useful for treating a neurodegenerative disorder.  
XX  
PS Claim 68; SEQ ID NO 3; 228pp; English.  
XX  
CC The invention relates to a novel medical system for treating a  
CC neurodegenerative disorder comprising an intracranial access device, a  
CC mapping means for locating a predetermined location in the brain, a  
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding  
CC the siRNA, and a delivery means. The system of the invention has  
CC applications related to the CNS and may be useful for treating a  
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
CC The current sequence is that of the sense DNA 2 encoding an siRNA  
CC targeted to human ataxin 1 mRNA of the invention.  
XX  
SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 90.5%; Score 19; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 TTCGTTGCTCCGCTCTTGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 TTCGTTGCTCCGCTCTTGG 3  
  
RESULT 4  
ADP44611/c  
ID ADP44611 standard; DNA; 21 BP.

```
XX ADP44611;
AC
XX
DT
XX
XX
DE
XX
XX
DE Sense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
XX
XX neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
KW Huntington's; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
KW small interfering RNA; ss; human; ataxin 1.
XX
XX Homo sapiens.
OS
XX
XX WO2004047872-A2.
PN
XX
XX 10-JUN-2004.
PD
XX
XX 26-NOV-2003; 2003WO-US037650.
XX
XX 26-NOV-2002; 2002US-0429387P.
XX
XX 03-FEB-2003; 2003US-0444614P.
XX
XX (MEDT ) MEDTRONIC INC.
PA
XX
XX Kaemmerer WF;
PI
XX
XX WPI; 2004-441106/41.
DR
XX
XX New medical system comprising an intracranial access device, a mapping
PT means, a small interfering RNA or vector encoding the RNA, and a delivery
PT means, useful for treating a neurodegenerative disorder.
XX
XX Claim 68; SEQ ID NO 1; 228pp; English.
XX
XX The invention relates to a novel medical system for treating a
CC neurodegenerative disorder comprising an intracranial access device, a
CC mapping means for locating a predetermined location in the brain, a
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
CC the siRNA, and a delivery means. The system of the invention has
CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the sense DNA 1 encoding an siRNA
CC targeted to human ataxin 1 mRNA of the invention.
XX
XX Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 90.5%; Score 19; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TTGCTTCTCCGCTCTTGG 21
Db 21 TTGCTTCTCCGCTCTTGG 3
RESULT 5
AAZ03368/c
ID AAZ03368 standard; DNA; 20 BP.
XX
XX AAZ03368;
AC
XX
XX 07-OCT-1999 (first entry)
DT
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
DE
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihemphatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
```

```
XX Synthetic.
OS Chlamydia trachomatis.
XX
XX WO9928475-A2.
PN
XX 10-JUN-1999.
PD
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX
XX 17-DEC-1997; 97FR-00016034.
XX
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
PA
XX
XX Griffais R;
PI
XX
XX WPI; 1999-371125/31.
DR
XX
XX Genome sequence of Chlamydia trachomatis.
PT
XX
XX Disclosure; Page 1601; 1755pp; English.
XX
XX PCR primers AAZ01426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihemphatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
XX diseases
XX
XX Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 57.1%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ATTCTGTTGCTCC 13
Db 13 ATTCTGTTGCTCC 2
RESULT 6
AAL48427
ID AAL48427 standard; DNA; 30 BP.
XX
XX AAL48427;
AC
XX
XX 03-OCT-2002 (first entry)
DT
XX
XX Secreted Chlamydia proteins related construct Inca/myCHIS PCR primer #2.
DE
XX
XX Chlamydia; secreted protein; type III secretion pathway; Inc; cya;
KW vaccine; chlamydial infection; antibacterial; antiatherosclerotic; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX Synthetic.
OS
XX WO200248185-A2.
PN
XX
XX 20-JUN-2002.
PD
XX
XX 13-DEC-2001; 2001WO-IB002808.
XX
XX 14-DEC-2000; 2000US-0255118P.
XX
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PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
XX  
XX PI Subtil A, Parsot C, Dautry-Varsat A;  
XX WPI; 2002-583484/62.  
DR  
XX Novel purified secreted Chlamydia polypeptide which is identified by its  
PT secretion in a Gram-negative bacterial strain containing a type III  
PT secretion pathway, useful for treating Chlamydia infections in humans.  
XX  
XX Example 1; Page 28; 57pp; English.  
XX  
CC The present invention relates to a purified secreted Chlamydia protein,  
CC which is identified by its expression by a Gram-negative bacterial strain  
CC and secretion by the type III secretion pathway of the bacterium. This  
CC can be used to diagnose, treat and vaccinate against Chlamydia infection  
CC in a patient, which may contribute to atherosclerosis or a sexually  
CC transmitted disease. The present sequence is a PCR primer used to produce  
CC fusion constructs in the exemplification of the invention  
XX  
XX Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 U; 0 Other;  
SQ

Query Match 57.1%; Score 12; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AATTCGTTGCTC 12  
DB 6 AATTCGTTGCTC 17

RESULT 7  
ADK96972/c  
ID ADK96972 standard; DNA; 19 BP.  
AC ADK96972;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Primer of the invention #2692.  
XX  
XX human; single nucleotide polymorphism; SNP; ss; primer.  
XX  
XX Synthetic.  
XX  
XX JP2003259875-A.  
XX  
XX 16-SEP-2003.  
XX  
XX 08-MAR-2002; 2002JP-00064373.  
XX  
XX 08-MAR-2002; 2002JP-00064373.  
XX  
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
XX WPI; 2004-093977/10.  
XX  
XX Novel polynucleotide useful for PCR amplification along with two DNA  
PT fragment from another set of sequences, or for detecting single  
PT nucleotide polymorphism in human gene.  
XX  
XX Claim 2; SEQ ID NO 6001; 2627pp; Japanese.  
XX  
XX The present invention relates to a polynucleotide isolated from a human  
CC gene and is useful for detecting a single nucleotide polymorphism in a  
CC human gene or for diagnosing of disease. The invention enables the  
CC detection of a single nucleotide polymorphism in a human gene. The  
CC present sequence represents a primer of the invention.  
XX  
XX Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TGCTCGCTCT 18  
DB 15 TGCTCGCTCT 5

RESULT 8  
AAK19405/c  
ID AAK19405 standard; DNA; 20 BP.  
XX  
XX AAK19405;  
XX  
XX 19-MAY-1999 (first entry)  
XX  
XX Neurogenin protein PCR forward primer.  
XX  
XX Secreted protein; microsome; signal peptide; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9905256-A2.  
XX  
XX 04-FEB-1999.  
XX  
XX 24-JUL-1998; 98WO-US015394.  
XX  
XX 24-JUL-1997; 97US-0053586P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Kirschner MW, Kinoshita N;  
PI WPI; 1999-153316/13.  
XX  
XX Isolating nucleic acids encoding proteins comprising a signal peptide -  
PT by translating RNA and isolating translated RNA that is associated with  
PT microsomes, useful as therapeutic agents.  
XX  
XX Example 2; Page 34; 45pp; English.  
XX  
XX The present invention describes the isolation of nucleic acid (I) that  
CC encodes a protein (II) having a signal peptide (SP), which comprises  
CC isolating RNA molecules (III) that are associated with microsomes under  
CC conditions where (III) is at least partly translated. Also described are:  
CC (1) a library of (I) encoding (II) comprising SP; (2) (I) isolated by the  
CC above method; and (3) (II) encoded by (I) (I) and (II) are useful  
CC therapeutically, typically (II) are cell growth factors such as  
CC cytokines, interleukins, colony-forming factors, possibly useful in  
CC treatment of cancer. (I) are also used; as tissue and molecular weight  
CC markers; as chromosome tags; to detect possible genetic disorders; as  
CC hybridisation probes to identify related nucleic acid; as primers for DNA  
CC fingerprinting; to generate antibodies; and in interaction trap assays to  
CC identify gene encoding specific binding agents. (II) are useful in drug  
CC screening, for raising antibodies (e.g. for use as immunoassay reagents)  
CC and to induce an immune response. The method is more efficient and  
CC reliable than the sequence trap system. It does not involve formation of  
CC a fusion protein (rather natural proteins are selected) and (II) do not  
CC have to be secreted. The present sequence represents a PCR primer which  
CC is used in an example from the present invention  
XX  
XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 CTCGCTCTTG 20  
DB 11 CTCGCTCTTG 1



RESULT 9  
AAZ04279/c  
ID AAZ04279 standard; DNA; 20 BP.  
XX AC AAZ04279;  
XX DT 07-OCT-1999 (first entry)  
XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
XX XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;  
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;  
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
XX OS Synthetic.  
OS Chlamydia trachomatis.  
XX PN WO9928475-A2.  
XX PD 10-JUN-1999.  
XX PF 27-NOV-1998; 98WO-IB001939.  
XX PR 28-NOV-1997; 97FR-00015041.  
XX PR 17-DEC-1997; 97FR-00016034.  
XX PR 04-NOV-1998; 98US-0107077P.  
XX PA (GEST ) GENSET.  
XX PI Griffais R;  
XX DR WPI; 1999-371125/31.  
XX PT Genome sequence of Chlamydia trachomatis.  
XX PS Disclosure; Page 1675; 1755pp; English.  
XX CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
CC be used to control growth of the microorganism. Chlamydia trachomatis is  
CC responsible for a large number of diseases, e.g. eye diseases such as  
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion  
CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;  
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
CC The polypeptides of the invention may be of use in treating these  
CC diseases  
XX SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 52.4%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TCCTTGCTCCG 14  
DB 15 TCCTTGCTCCG 5  
RESULT 10  
AAZ55953/c  
ID AAZ55953 standard; cDNA; 20 BP.  
XX AC AAZ55953;  
XX DT 10-APR-2000 (first entry)  
XX DE Xenopus laevis neurogenin sense PCR primer, SEQ ID NO:31.  
XX

KW Neurogenin; Zic3; zinc finger; neuroregeneration; neurological disease;  
KW diagnosis; Alzheimer's disease; expression pattern; PCR primer; ss.  
OS Xenopus laevis.  
XX PN JP11341985-A.  
XX PD 14-DEC-1999.  
XX PF 30-APR-1998; 98JP-00121456.  
XX PR 31-MAR-1998; 98JP-00086979.  
XX PA (RIKA ) RIKAGAKU KENKYUSHO.  
XX DR WPI; 2000-101694/09.  
XX PT A nerve formation-inducing gene - useful as a diagnostic agent for  
XX nervous diseases, and for treating Alzheimer disease.  
XX PS Example 2; Page 14; 30pp; Japanese.  
XX CC The invention relates to Xenopus laevis Zic3 protein (AAV69524). Zic3  
CC contains a zinc finger motif, and induces the formation of neurons. The  
CC cDNA was obtained from embryonic Xenopus nerve poly(A+) RNA. Zic3, and  
CC nucleotides encoding it, are useful as diagnostic tools for neurological  
CC diseases, and for the treatment of Alzheimer's disease. Sequences  
CC AAZ55931-255962 represent PCR primers used to determine which other genes  
CC are expressed with Zic3 in various Xenopus cell types in an  
XX exemplification of the present invention  
XX SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 52.4%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 CTCGCGCTCTTG 20  
DB 11 CTCGCGCTCTTG 1  
RESULT 11  
AAZ23328  
ID AAZ23328 standard; DNA; 20 BP.  
XX AC AAZ23328;  
XX DT 19-MAR-2001 (first entry)  
XX DE Oligonucleotide for detection of Mycobacterium porcinum.  
XX KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;  
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;  
KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;  
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;  
KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.  
OS Mycobacterium porcinum.  
XX PN WO200073436-A1.  
XX PD 07-DEC-2000.  
XX PF 16-MAY-2000; 2000WO-KR000477.  
XX PR 29-MAY-1999; 99KR-00019631.  
XX PR 29-MAY-1999; 99KR-00019632.  
XX PR 29-MAY-1999; 99KR-00019633.  
XX PR 29-MAY-1999; 99KR-00019634.  
XX PR 29-MAY-1999; 99KR-00019635.  
XX PR 07-APR-2000; 2000KR-00018189.  
XX

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PA (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
XX Kim CM, Park HK, Jang HU;
XX WPI; 2001-061527/07.
XX
XX Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
XX Claim 34; Page 78; 89pp; English.
XX
XX The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC diernhoferi genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
XX Sequence 20 BP; 0 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GTTGCTCCGCT 16
DB 10 GTTGCTCCGCT 20
RESULT 12
ADD56623
ID - ADD56623 standard; DNA; 20 BP.
XX
XX ADD56623;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human gene expression analysis multiplex Start-PCR primer #143.
XX
XX Gene expression; multiplex standardised reverse transcriptase-PCR;
XX Start-PCR; high density oligonucleotide array; cDNA array;
XX Small biological sample; fine needle aspirate biopsy;
XX laser captured microdissected material; human; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003186246-A1.
XX
XX 02-OCT-2003.
XX
XX 28-MAR-2002; 2002US-00109349.
XX
XX 28-MAR-2002; 2002US-00109349.
XX
XX (WILL/) WILLEY J C.
XX PA (CRAW/) CRAWFORD E L.
XX
XX Willey JC, Crawford EL;
WPI; 2003-811730/76.
Direct comparison of numerical gene expression values between samples of
PT genes comprises using multiplex standardized reverse transcription-
PT polymerase chain reaction.
XX
XX Example 1; SEQ ID NO 143; 59pp; English.
XX
XX The present invention relates to a method for the direct comparison of
CC numerical gene expression values between samples of genes. The method
CC comprises amplifying cDNA in the presence of a competitive template
CC mixture and primer pairs for several genes and then amplifying aliquots
CC of the PCR products using a primer pair specific for each gene. The
CC method of amplification is by multiplex standardised reverse
CC transcriptase-polymerase chain reaction (Start-PCR). High density
CC oligonucleotide or cDNA arrays are used to measure PCR products following
CC quantitative Start-PCR. The method is useful for the assessment of gene
CC expression in small biological samples such as fine needle aspirate
CC biopsies, and laser captured microdissected materials. The method allows
CC for the standardised measurement of hundreds of genes from the same
CC sample, which in prior art, could only be assessed for one gene. The
CC present sequence represents a multiplex Start-PCR primer which can be
CC used in the method of the present invention.
XX
XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 TTCGTGCTCC 13
DB 8 TTCGTGCTCC 18
RESULT 13
AB297696
ID AB297696 standard; DNA; 20 BP.
XX
XX AB297696;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human CCR3 oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; lung; adenosine sensitivity;
XX lung inflammation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

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PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12938; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 TTGCTCCGCTC 17
DB 1 TTGCTCCGCTC 11
RESULT 14
ABZ97695
ID ABZ97695 standard; DNA; 20 BP.
XX
AC ABZ97695;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human CCR3 oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; db.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

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```

PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12937; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 TTGCTCCGCTC 17
DB 6 TTGCTCCGCTC 16
RESULT 15
ABD30726
ID ABD30726 standard; DNA; 20 BP.
XX
AC ABD30726;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human CCR3-derived oligonucleotide SEQ ID 12937.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense

```

PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 12937; 763pp; English.

XX  
CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX  
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCGGCTC 17

DB 6 TTGCTCGGCTC 16

Search completed: September 12, 2005, 17:04:31

Job time : 175 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 14:04:18 ; Search time 174 Seconds  
(without alignments)  
714.452 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aacaaagagcggagcaacgaa 21

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2557800

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	12 ADP44613	Adp44613 Sense DNA
2	21	100.0	21	12 ADP44611	Adp44611 Sense DNA
C 3	19	90.5	21	12 ADP44614	Adp44614 Antisense
C 4	19	90.5	21	12 ADP44612	Adp44612 Antisense
C 5	12	57.1	25	9 AC135330	Ac135330 Human mic
6	11	52.4	19	12 ADK96972	Adk96972 Primer of
7	11	52.4	20	2 AAX19405	Aax19405 Neurogeni
8	11	52.4	20	2 AAZ03368	Aaz03368 PCR prime
9	11	52.4	20	2 AAZ04279	Aaz04279 PCR prime
10	11	52.4	20	3 AAZ55953	Aaz55953 Xenopus l
C 11	11	52.4	20	4 AAF23328	Aaf23328 Oligonuc1
C 12	11	52.4	20	10 ADS56623	Ads56623 Human gen
C 13	11	52.4	20	10 ABZ97696	Abz97696 Human CCR
C 14	11	52.4	20	10 ABZ97695	Abz97695 Human CCR
C 15	11	52.4	20	11 ABD30726	Abd30726 Human CCR
C 16	11	52.4	20	11 ABD30727	Abd30727 Human CCR
C 17	11	52.4	20	12 ADJ59552	Adj59552 Oligonuc1
C 18	11	52.4	20	12 ADJ59553	Adj59553 Oligonuc1
C 19	11	52.4	20	12 ADO45043	Ado45043 Human oli
C 20	11	52.4	20	12 ADO45042	Ado45042 Human oli

C 21	11	52.4	24	4 AAI69892	Aai69892 Human rib
C 22	11	52.4	25	6 ABQ87970	Abq87970 Enterohae
C 23	11	52.4	29	2 AAQ84819	Aaq84819 Spinocere
24	11	52.4	29	2 AAX80489	Aax80489 Human sec
25	11	52.4	29	4 AAS59324	Aas59324 Human sec
26	11	52.4	29	6 ABA90993	Abas90993 Biotinyla
27	11	52.4	29	12 ADO61037	Ado61037 Human deb
C 28	11	52.4	30	12 ADP80578	Adp80578 Novel mic
C 29	10	47.6	16	4 AAS00058	Aas00058 Synthetic
30	10	47.6	17	2 AAV42302	Aav42302 Primer us
C 31	10	47.6	17	2 AAV96406	Aav96406 Potato ci
C 32	10	47.6	17	2 AAV96405	Aav96405 Potato ci
C 33	10	47.6	17	6 ABS97488	Abs97488 Human epo
C 34	10	47.6	17	6 ACN01300	Acn01300 WNV Hamme
C 35	10	47.6	17	6 ACN12384	Acn12384 WNV minus
36	10	47.6	17	6 ACN14271	Acn14271 WNV minus
C 37	10	47.6	17	6 ACN04597	Acn04597 WNV Zinzy
38	10	47.6	17	6 ACN14270	Acn14270 WNV minus
C 39	10	47.6	17	6 ACN03280	Acn03280 WNV Inozy
C 40	10	47.6	17	6 ACN04596	Acn04596 WNV Zinzy
41	10	47.6	17	6 ACN12383	Acn12383 WNV minus
C 42	10	47.6	17	6 ACN01301	Acn01301 WNV Hamme
C 43	10	47.6	17	6 ACN03279	Acn03279 WNV Inozy
44	10	47.6	17	6 ACN09757	Acn09757 WNV minus
45	10	47.6	17	10 ADI49330	Adi49330 Human tum

ALIGNMENTS

RESULT 1  
ADP44613  
ID ADP44613 standard; DNA; 21 BP.  
AC ADP44613;

DT 26-AUG-2004 (first entry)

Sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.

neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;  
Huntington's; spinocerebellar ataxia type 1;  
spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;  
dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;  
small interfering RNA; ss; human; ataxin 1.

OS Homo sapiens.

PN WO2004047872-A2.

PD 10-JUN-2004.

PF 26-NOV-2003; 2003WO-US037650.

PR 26-NOV-2002; 2002US-0429387P.

XX 03-FEB-2003; 2003US-0444614P.

PA (MEDT ) MEDTRONIC INC.

XX Kaemmerer WF;

PI WPI; 2004-441106/41.

DR New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.

XX Claim 68; SEQ ID NO 3; 228bp; English.

CC The invention relates to a novel medical system for treating a neurodegenerative disorder comprising an intracranial access device, a mapping means for locating a predetermined location in the brain, a deliverable amount of a small interfering RNA (siRNA), or vector encoding

CC the siRNA, and a delivery means. The system of the invention has  
 CC applications related to the CNS and may be useful for treating a  
 CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
 CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
 CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
 CC The current sequence is that of the sense DNA 2 encoding an siRNA  
 CC targeted to human ataxin 1 mRNA of the invention.

XX SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 21; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGAGCAACGAA 21  
 |||||  
 Db 1 AACCAAGAGCGGAGCAACGAA 21  
 |||||

RESULT 2  
 ADP44611  
 ID ADP44611 standard; DNA; 21 BP.  
 XX AC ADP44611;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Sense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.  
 XX KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;  
 KW Huntington's; spinocerebellar ataxia type 1;  
 KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;  
 KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;  
 KW small interfering RNA; ss; human; ataxin 1.  
 XX OS Homo sapiens.  
 XX PN WO2004047872-A2.  
 XX PD 10-JUN-2004.  
 XX PF 26-NOV-2003; 2003WO-US037650.  
 XX PR 26-NOV-2002; 2002US-0429387P.  
 XX PR 03-FEB-2003; 2003US-0444614P.  
 XX PA (MEDT ) MEDTRONIC INC.  
 XX PI Kaemmerer WF;  
 XX DR WPI; 2004-441106/41.  
 XX PT New medical system comprising an intracranial access device, a mapping  
 PT means, a small interfering RNA or vector encoding the RNA, and a delivery  
 PT means, useful for treating a neurodegenerative disorder.  
 XX PS Claim 68; SEQ ID NO 1; 228pp; English.  
 XX CC The invention relates to a novel medical system for treating a  
 CC neurodegenerative disorder comprising an intracranial access device, a  
 CC mapping means for locating a predetermined location in the brain, a  
 CC deliverable amount of a small interfering RNA (siRNA), or vector encoding  
 CC the siRNA, and a delivery means. The system of the invention has  
 CC applications related to the CNS and may be useful for treating a  
 CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
 CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
 CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
 CC The current sequence is that of the sense DNA 1 encoding an siRNA  
 CC targeted to human ataxin 1 mRNA of the invention.

XX SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 21; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGAGCAACGAA 21  
 |||||  
 Db 1 AACCAAGAGCGGAGCAACGAA 21  
 |||||

Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGAGCAACGAA 21  
 |||||  
 Db 1 AACCAAGAGCGGAGCAACGAA 21  
 |||||

RESULT 3  
 ADP44614/c  
 ID ADP44614 standard; DNA; 21 BP.  
 XX AC ADP44614;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Antisense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.  
 XX KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;  
 KW Huntington's; spinocerebellar ataxia type 1;  
 KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;  
 KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;  
 KW small interfering RNA; ss; human; ataxin 1.  
 XX OS Homo sapiens.  
 XX PN WO2004047872-A2.  
 XX PD 10-JUN-2004.  
 XX PF 26-NOV-2003; 2003WO-US037650.  
 XX PR 26-NOV-2002; 2002US-0429387P.  
 XX PR 03-FEB-2003; 2003US-0444614P.  
 XX PA (MEDT ) MEDTRONIC INC.  
 XX PI Kaemmerer WF;  
 XX DR WPI; 2004-441106/41.  
 XX PT New medical system comprising an intracranial access device, a mapping  
 PT means, a small interfering RNA or vector encoding the RNA, and a delivery  
 PT means, useful for treating a neurodegenerative disorder.  
 XX PS Claim 68; SEQ ID NO 4; 228pp; English.  
 XX CC The invention relates to a novel medical system for treating a  
 CC neurodegenerative disorder comprising an intracranial access device, a  
 CC mapping means for locating a predetermined location in the brain, a  
 CC deliverable amount of a small interfering RNA (siRNA), or vector encoding  
 CC the siRNA, and a delivery means. The system of the invention has  
 CC applications related to the CNS and may be useful for treating a  
 CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's  
 CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3  
 CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).  
 CC The current sequence is that of the antisense DNA 2 encoding an siRNA  
 CC targeted to human ataxin 1 mRNA of the invention.

XX SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;  
 Query Match 90.5%; Score 19; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAAGAGCGGAGCAACGAA 21  
 |||||  
 Db 21 CCAAGAGCGGAGCAACGAA 3  
 |||||

RESULT 4  
 ADP44612/c  
 ID ADP44612 standard; DNA; 21 BP.

```

XX AC ADP44612;
XX XX
XX DT 26-AUG-2004 (first entry)
XX XX
XX DE Antisense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
XX XX
XX KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
XX KW Huntington's; spinocerebellar ataxia type 1;
XX KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
XX KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
XX KW small interfering RNA; ss; human; ataxin 1.
XX OS
XX XX Homo sapiens.
XX XX
XX PN WO2004047872-A2.
XX XX
XX PD 10-JUN-2004.
XX XX
XX PF 26-NOV-2003; 2003WO-US037650.
XX XX
XX PR 26-NOV-2002; 2002US-0429387P.
XX PR 03-FEB-2003; 2003US-0444614P.
XX XX
XX PA (MEDT ) MEDTRONIC INC.
XX XX
XX PI Kaemmerer WF;
XX XX
XX DR WPI; 2004-441106/41.
XX XX
XX PT New medical system comprising an intracranial access device, a mapping
XX PT means, a small interfering RNA or vector encoding the RNA, and a delivery
XX PT means, useful for treating a neurodegenerative disorder.
XX XX
XX PS Claim 68; SEQ ID NO 2; 228pp; English.
XX XX
XX CC The invention relates to a novel medical system for treating a
XX CC neurodegenerative disorder comprising an intracranial access device, a
XX CC mapping means for locating a predetermined location in the brain, a
XX CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
XX CC the siRNA, and a delivery means. The system of the invention has
XX CC applications related to the CNS and may be useful for treating a
XX CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
XX CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
XX CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
XX CC The current sequence is that of the antisense DNA 1 encoding an siRNA
XX CC targeted to human ataxin 1 mRNA of the invention.
XX SQ
XX Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 90.5%; Score 19; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCAAGAGCGGAGCAACGAA 21
Db 21 CCAAGAGCGGAGCAACGAA 3
RESULT 5
ACI35330/c
ID ACI35330 standard; DNA; 25 BP.
XX XX
XX AC ACI35330;
XX XX
XX DT 13-OCT-2003 (first entry)
XX XX
XX DE Human microarray DNA oligonucleotide SEQ ID NO 35321.
XX XX
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX XX

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OS Homo sapiens.
XX XX
XX PN US2003104410-A1.
XX XX
XX PD 05-JUN-2003.
XX XX
XX PF 15-MAR-2002; 2002US-00098263.
XX XX
XX PR 16-MAR-2001; 2001US-0276759P.
XX XX
XX PA (AFFY-) AFFMETRIX INC.
XX XX
XX PI Mittmann MP;
XX XX
XX DR WPI; 2003-567953/53.
XX XX
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX XX
XX PS Claim 1; SEQ ID NO 35321; 9pp; English.
XX XX
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX SQ
XX Sequence 25 BP; 2 A; 5 C; 6 G; 12 T; 0 U; 0 Other;
Query Match 57.1%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACCAAGAGCGG 12
Db 14 AACCAAGAGCGG 3
RESULT 6
ADK96972
ID ADK96972 standard; DNA; 19 BP.
XX XX
XX AC ADK96972;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE Primer of the invention #2692.
XX XX
XX KW human; single nucleotide polymorphism; SNP; ss; primer.
XX XX
XX OS Synthetic.
XX XX
XX PN JP2003259875-A.
XX XX

```

PD 16-SEP-2003.  
 XX  
 PF 08-MAR-2002; 2002JP-00064373.  
 XX  
 PR 08-MAR-2002; 2002JP-00064373.  
 XX  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX  
 DR WPI; 2004-093977/10.  
 XX  
 PT Novel polynucleotide useful for PCR amplification along with two DNA  
 PT fragment from another set of sequences, or for detecting single  
 PT nucleotide polymorphism in human gene.  
 XX  
 PS Claim 2; SEQ ID NO 6001; 2627pp; Japanese.  
 XX  
 CC The present invention relates to a polynucleotide isolated from a human  
 CC gene and is useful for detecting a single nucleotide polymorphism in a  
 CC human gene or for diagnosing of disease. The invention enables the  
 CC detection of a single nucleotide polymorphism in a human gene. The  
 CC present sequence represents a primer of the invention.  
 XX  
 SQ Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 52.4%; Score 11; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 AGAGCGGAGCA 16  
 Db |||||  
 5 AGAGCGGAGCA 15  
 RESULT 7  
 AAX19405  
 ID AAX19405 standard; DNA; 20 BP.  
 XX  
 AC AAX19405;  
 XX  
 DT 19-MAY-1999 (first entry)  
 XX  
 DE Neurogenin protein PCR forward primer.  
 XX  
 KW Secreted protein; microsome; signal peptide; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9905256-A2.  
 XX  
 PD 04-FEB-1999.  
 XX  
 PF 24-JUL-1998; 98WO-US015394.  
 XX  
 PR 24-JUL-1997; 97US-0053586P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Kirschner MW, Kinoshita N;  
 XX  
 DR WPI; 1999-153316/13.  
 XX  
 PT Isolating nucleic acids encoding proteins comprising a signal peptide -  
 PT by translating RNA and isolating translated RNA that is associated with  
 PT microsomes, useful as therapeutic agents.  
 XX  
 PS Example 2; Page 34; 45pp; English.  
 XX  
 CC The present invention describes the isolation of nucleic acid (I) that  
 CC encodes a protein (II) having a signal peptide (SP), which comprises  
 CC isolating RNA molecules (III) that are associated with microsomes under  
 CC conditions where (III) is at least partly translated. Also described are:  
 CC (1) a library of (I) encoding (II) comprising SP; (2) (I) isolated by the  
 CC above method; and (3) (II) encoded by (I). (I) and (II) are useful

CC therapeutically, typically (II) are cell growth factors such as  
 CC cytokines, interleukins, colony-forming factors, possibly useful in  
 CC treatment of cancer. (I) are also used: as tissue and molecular weight  
 CC markers; as chromosome tags; to detect possible genetic disorders; as  
 CC hybridisation probes to identify related nucleic acid; as primers for DNA  
 CC fingerprinting; to generate antibodies; and in interaction trap assays to  
 CC identify gene encoding specific binding agents. (II) are useful in drug  
 CC screening, for raising antibodies (e.g. for use as immunoassay reagents)  
 CC and to induce an immune response. The method is more efficient and  
 CC reliable than the sequence trap system. It does not involve formation of  
 CC a fusion protein (rather natural proteins are selected) and (II) do not  
 CC have to be secreted. The present sequence represents a PCR primer which  
 CC is used in an example from the present invention  
 XX  
 SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 52.4%; Score 11; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CAAGAGCGGAG 14  
 Db |||||  
 1 CAAGAGCGGAG 11  
 RESULT 8  
 AAZ03368  
 ID AAZ03368 standard; DNA; 20 BP.  
 XX  
 AC AAZ03368;  
 XX  
 DT 07-OCT-1999 (first entry)  
 XX  
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
 XX  
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;  
 KW paratrachoma; inclusion conjunctivitis; genital disease; perinephritis;  
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
 XX  
 OS Synthetic.  
 OS Chlamydia trachomatis.  
 XX  
 PN WO9928475-A2.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 27-NOV-1998; 98WO-IB001939.  
 XX  
 PR 28-NOV-1997; 97FR-00015041.  
 PR 17-DEC-1997; 97FR-00016034.  
 PR 04-NOV-1998; 98US-0107077P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Griffais R;  
 XX  
 DR WPI; 1999-371125/31.  
 XX  
 PT Genome sequence of Chlamydia trachomatis.  
 XX  
 PS Disclosure; Page 1601; 1755pp; English.  
 XX  
 CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
 CC be used to control growth of the microorganism. Chlamydia trachomatis is  
 CC responsible for a large number of diseases, e.g. eye diseases such as  
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion  
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
 CC epididymitis, cervicitis, salpingitis, perinephritis, Bartholinitis;  
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.



CC The polypeptides of the invention may be of use in treating these

CC

CC diseases

SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAGCAACGAA 21

|||||

Db 2 GGAGCAACGAA 12

RESULT 9

AAZ04279

ID AAZ04279 standard; DNA; 20 BP.

XX

AC AAZ04279;

XX

DT 07-OCT-1999 (first entry)

XX

DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;  
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;  
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX

OS Synthetic.

OS

OS Chlamydia trachomatis.

XX

PN WO9928475-A2.

XX

PD 10-JUN-1999.

XX

PF 27-NOV-1998; 98WO-IB001939.

XX

PR 28-NOV-1997; 97FR-00015041.

XX

PR 17-DEC-1997; 97FR-00016034.

XX

PR 04-NOV-1998; 98US-0107077P.

XX

PA (GEST ) GENSET.

XX

PI Griffais R;

XX

DR WPI; 1999-371125/31.

XX

PT Genome sequence of Chlamydia trachomatis.

XX

PS Disclosure; Page 1675; 1755pp; English.

XX

CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
(ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
encode polypeptides (see AAZ36754-Y37949) which can be used as vaccines  
against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
be used to control growth of the microorganism. Chlamydia trachomatis is  
responsible for a large number of diseases, e.g. eye diseases such as  
conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion  
conjunctivitis; genital diseases such as nongonococcal urethritis,  
epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;  
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
CC The polypeptides of the invention may be of use in treating these  
CC diseases

XX

SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGGAGCAACGA 20

|||||

Db 5 CGGAGCAACGA 15

RESULT 10

AAZ55953

ID AAZ55953 standard; cDNA; 20 BP.

XX

AC AAZ55953;

XX

DT 10-APR-2000 (first entry)

XX

DE Xenopus laevis neurogenin sense PCR primer, SEQ ID NO:31.

XX

KW Neurogenin; Zic3; zinc finger; neuroregeneration; neurological disease;  
KW diagnosis; Alzheimer's disease; expression pattern; PCR primer; ss.

XX

OS Xenopus laevis.

OS

PN JP11341985-A.

XX

PD 14-DEC-1999.

XX

PF 30-APR-1998; 98JP-00121456.

XX

PR 31-MAR-1998; 98JP-00086979.

XX

PA (RIKA ) RIKAGAKU KENKYUSHO.

XX

DR WPI; 2000-101694/09.

XX

PT A nerve formation-inducing gene - useful as a diagnostic agent for  
nervous diseases, and for treating Alzheimer disease.

XX

PS Example 2; Page 14; 30pp; Japanese.

XX

CC The invention relates to Xenopus laevis Zic3 protein (AAZ69524). Zic3  
contains a zinc finger motif, and induces the formation of neurons. The  
cDNA was obtained from embryonic Xenopus nerve poly(A+) RNA. Zic3, and  
CC nucleotides encoding it, are useful as diagnostic tools for neurological  
diseases, and for the treatment of Alzheimer's disease. Sequences  
CC AAZ5931-Z55962 represent PCR primers used to determine which other genes  
CC are expressed with Zic3 in various Xenopus cell types in an  
CC exemplification of the present invention

XX

SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAAGAGCGGAG 14

|||||

Db 1 CAAGAGCGGAG 11

RESULT 11

AAZ23328/c

ID AAZ23328 standard; DNA; 20 BP.

XX

AC AAZ23328;

XX

DT 19-MAR-2001 (first entry)

XX

DE Oligonucleotide for detection of Mycobacterium porcinum.

XX

KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;  
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;  
KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;  
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;  
KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.

XX

OS Mycobacterium porcinum.

XX

```

PN WO200073436-A1.
XX
PD
XX
XX
XX PF 07-DEC-2000.
XX
XX 16-MAY-2000; 2000WO-KR000477.
XX
XX 29-MAY-1999; 99KR-00019631.
XX PR 29-MAY-1999; 99KR-00019632.
XX PR 29-MAY-1999; 99KR-00019633.
XX PR 29-MAY-1999; 99KR-00019634.
XX PR 29-MAY-1999; 99KR-00019635.
XX PR 07-APR-2000; 2000KR-00018189.
XX
XX (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
XX Kim CM, Park HK, Jang HJ;
XX
XX WPI; 2001-061527/07.
XX
XX Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
XX Claim 34; Page 78; 89pp; English.
XX
XX The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC thermohofri genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
XX Sequence 20 BP; 0 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGCGGAGCAAC 18
Db 20 AGCGGAGCAAC 10
|||||
|

RESULT 12
ADD56623/C
ID ADD56623 standard; DNA; 20 BP.
XX
XX ADD56623;
AC
XX 15-JAN-2004 (first entry)
DT
XX Human gene expression analysis multiplex Start-PCR primer #143.
DE
XX Gene expression; multiplex standardised reverse transcriptase-PCR;
KW Start-PCR; high density oligonucleotide array; cDNA array;
KW small biological sample; fine needle aspirate biopsy;
KW laser captured microdissected material; human; primer; ss.
XX
XX Homo sapiens.
OS

US2003186246-A1.
XX
XX 02-OCT-2003.
XX
XX 28-MAR-2002; 2002US-00109349.
XX
XX 28-MAR-2002; 2002US-00109349.
XX (WILL/) WILLEY J C.
PA (CRAW/) CRAWFORD E L.
XX
XX Willey JC, Crawford EL;
XX
XX WPI; 2003-811730/76.
XX
XX Direct comparison of numerical gene expression values between samples of
PT genes comprises using multiplex standardised reverse transcription-
PT polymerase chain reaction.
XX
XX Example 1; SEQ ID NO 143; 59pp; English.
XX
XX The present invention relates to a method for the direct comparison of
CC numerical gene expression values between samples of genes. The method
CC comprises amplifying cDNA in the presence of a competitive template
CC mixture and primer pairs for several genes and then amplifying aliquots
CC of the PCR products using a primer pair specific for each gene. The
CC method of amplification is by multiplex standardised reverse
CC transcriptase-polymerase chain reaction (Start-PCR). High density
CC oligonucleotide or cDNA arrays are used to measure PCR products following
CC quantitative Start-PCR. The method is useful for the assessment of gene
CC expression in small biological samples such as fine needle aspirate
CC biopsies, and laser captured microdissected materials. The method allows
CC for the standardised measurement of hundreds of genes from the same
CC sample, which in prior art, could only be assessed for one gene. The
CC present sequence represents a multiplex Start-PCR primer which can be
CC used in the method of the present invention.
XX
XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGAGCGACGAA 21
Db 18 GGAGCGACGAA 8
|||||
|

RESULT 13
ABZ97696/C
ID ABZ97696 standard; DNA; 20 BP.
XX
XX ABZ97696;
AC
XX 17-OCT-2003 (first entry)
DT
XX Human CCR3 oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF

```

```

XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12938; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCGGAGCAA 17
Db |||||
11 GAGCGGAGCAA 1

RESULT 14
ABZ97695/c
XX ID ABZ97695 standard; DNA; 20 BP.
XX AC ABZ97695;
XX XX
XX DT 17-OCT-2003 (first entry)
XX DE Human CCR3 oligonucleotide sequence.
XX XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX XX
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX XX
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12937; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCGGAGCAA 17
Db |||||
16 GAGCGGAGCAA 6

RESULT 15
ABD30726/c
XX ID ABD30726 standard; DNA; 20 BP.
XX AC ABD30726;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Human CCR3-derived oligonucleotide SEQ ID 12937.
XX XX
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX KW pulmonary transplantation rejection; ss; primer.
XX XX
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX XX
XX PD 31-OCT-2002.
XX PF 31-OCT-2002.

```

XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-093058/08.  
DR  
XX Pharmaceutical composition for treating asthma, has antisense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
PT  
XX Claim 15; SEQ ID NO 12937; 763pp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 52.4%; Score 11; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 GAGCGGAGCAA 17  
Db 16 GAGCGGAGCAA 6  
|||||

Search completed: September 12, 2005, 17:04:30  
Job time : 179 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005., 16:58:36 ; Search time 278.5 Seconds  
(without alignments)  
495.196 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21  
Sequence: 1 aaccaagagcgagcaacgaa 21

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7001036

Minimum DB seq length: 15  
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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- 4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:\*
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- 13: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:\*
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- 19: /cgn2\_6/prodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/prodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/prodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	21	100.0	21	19	US-10-721-693-3
3	21	100.0	21	20	US-10-852-997-1
4	21	100.0	21	20	US-10-852-997-3
C 5	19	90.5	21	19	US-10-721-693-2
C 6	19	90.5	21	19	US-10-721-693-4
C 7	19	90.5	21	20	US-10-852-997-2

C 8	19	90.5	21	20	US-10-852-997-4	Sequence 4, Appli
C 9	13	61.9	25	21	US-10-809-189-18110	Sequence 18110, A
C 10	13	61.9	25	21	US-10-809-189-18111	Sequence 18111, A
C 11	13	61.9	25	22	US-10-719-956-201094	Sequence 201094, A
C 12	13	61.9	25	22	US-10-719-956-425371	Sequence 425371, A
C 13	12	57.1	25	15	US-10-098-263B-35321	Sequence 35321, A
C 14	12	57.1	25	21	US-10-719-900-49468	Sequence 49468, A
C 15	12	57.1	25	21	US-10-719-900-272193	Sequence 272193, A
C 16	12	57.1	25	21	US-10-719-900-399511	Sequence 399511, A
C 17	12	57.1	25	21	US-10-719-900-548718	Sequence 548718, A
C 18	12	57.1	25	21	US-10-719-900-911843	Sequence 911843, A
C 19	12	57.1	25	21	US-10-719-900-911844	Sequence 911844, A
C 20	12	57.1	25	21	US-10-719-900-950357	Sequence 950357, A
C 21	12	57.1	25	21	US-10-719-900-978443	Sequence 978443, A
C 22	12	57.1	25	21	US-10-719-956-157-278869	Sequence 278869, A
C 23	12	57.1	25	22	US-10-719-956-202563	Sequence 202563, A
C 24	12	57.1	25	22	US-10-719-956-573056	Sequence 573056, A
C 25	11	52.4	20	15	US-10-244-367-31	Sequence 31, Appli
C 26	11	52.4	20	16	US-10-109-349A-143	Sequence 143, App
C 27	11	52.4	20	17	US-10-448-836-202	Sequence 202, App
C 28	11	52.4	20	17	US-10-448-914A-202	Sequence 202, App
C 29	11	52.4	21	20	US-10-751-736-14580	Sequence 14580, A
C 30	11	52.4	21	20	US-10-751-736-19971	Sequence 19971, A
C 31	11	52.4	21	20	US-10-751-736-20001	Sequence 20001, A
C 32	11	52.4	21	20	US-10-751-736-46366	Sequence 46366, A
C 33	11	52.4	22	20	US-10-751-736-46367	Sequence 46367, A
C 34	11	52.4	22	21	US-10-933-611-11	Sequence 11, Appli
C 35	11	52.4	22	21	US-10-933-611-12	Sequence 12, Appli
C 36	11	52.4	22	21	US-10-933-611-15	Sequence 15, Appli
C 37	11	52.4	22	21	US-10-933-611-16	Sequence 16, Appli
C 38	11	52.4	25	19	US-10-250-997-69	Sequence 69, Appli
C 39	11	52.4	25	21	US-10-719-900-142642	Sequence 142642, A
C 40	11	52.4	25	21	US-10-719-900-206389	Sequence 206389, A
C 41	11	52.4	25	21	US-10-719-900-248436	Sequence 248436, A
C 42	11	52.4	25	21	US-10-719-900-256115	Sequence 256115, A
C 43	11	52.4	25	21	US-10-719-900-290010	Sequence 290010, A
C 44	11	52.4	25	21	US-10-719-900-297061	Sequence 297061, A
C 45	11	52.4	25	21	US-10-719-900-297062	Sequence 297062, A

#### ALIGNMENTS

RESULT 1  
US-10-721-693-1  
; Sequence 1, Application US/10721693  
; Publication No. US20040162255A1  
; GENERAL INFORMATION:  
; APPLICANT: Medtronic, Inc.  
; APPLICANT: Kaemmerer, William F.  
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv  
; TITLE OF INVENTION: siRNA  
; FILE REFERENCE: P11089.00  
; CURRENT APPLICATION NUMBER: US/10/721,693  
; CURRENT FILING DATE: 2003-11-25  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1.  
; SEQ ID NO 1  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-721-693-1

Query Match 100.0%; Score 21; DB 19; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGAGCGGAGCAACGAA 21  
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Db 1 AACCAAGAGCGGAGCAACGAA 21

RESULT 2

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US-10-721-693-3
; Sequence 3, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-3
Query Match      100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
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RESULT 3
US-10-852-997-1
; Sequence 1, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-1
Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
|||||
US-10-721-693-3
; Sequence 3, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-3
Query Match      100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
|||||
RESULT 3
US-10-852-997-1
; Sequence 1, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-1
Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
|||||
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US-10-721-693-3
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-3
Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
|||||
RESULT 5
US-10-721-693-2/c
; Sequence 2, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-2
Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 CCAAGAGCGGAGCAACGAA 21
Db      21 CCAAGAGCGGAGCAACGAA 3
|||||
RESULT 6
US-10-721-693-4/c
; Sequence 4, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-4
Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 CCAAGAGCGGAGCAACGAA 21
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Db 21 CCAAGAGCGGAGCAACGAA 3
|||||
RESULT 7
US-10-852-997-2/c
; Sequence 2, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; PRIOR FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-2
Query Match 90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAAGAGCGGAGCAACGAA 21
|||||
Db 21 CCAAGAGCGGAGCAACGAA 3

RESULT 8
US-10-852-997-4/c
; Sequence 4, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR FILING DATE: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-4
Query Match 90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAAGAGCGGAGCAACGAA 21
|||||
Db 21 CCAAGAGCGGAGCAACGAA 3

RESULT 9
US-10-809-189-18110/c
; Sequence 18110, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
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; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18110
Query Match 61.9%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGA 13
|||||
Db 21 AACCAAGAGCGGA 9

RESULT 10
US-10-809-189-18111/c
; Sequence 18111, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18111
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18111
Query Match 61.9%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGA 13
|||||
Db 13 AACCAAGAGCGGA 1

RESULT 11
US-10-719-956-201094/c
; Sequence 201094, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 16:40:43 ; Search time 58 Seconds  
(without alignments)  
592.445 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aaccaagagcgagcaacgaa 21

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Gapop\_60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

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Total number of hits satisfying chosen parameters: 914340

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA:\*

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- 2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/1/ina/PCRUS COMB.seq.\*
- 6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	13	61.9	25	4	US-09-396-196G-18111
C 3	11	52.4	20	3	US-09-121-920-26
C 4	11	52.4	20	3	US-09-172-045-31
C 5	11	52.4	20	4	US-09-342-325C-31
C 6	11	52.4	20	4	US-09-980-052-202
C 7	11	52.4	22	4	US-09-332-522B-81
C 8	11	52.4	25	4	US-09-396-196G-14051
C 9	11	52.4	25	4	US-09-396-196G-18094
C 10	11	52.4	25	4	US-09-396-196G-18109
C 11	11	52.4	25	4	US-09-396-196G-66426
C 12	11	52.4	25	4	US-09-396-196G-66427
C 13	11	52.4	25	4	US-09-396-196G-66438
C 14	11	52.4	29	2	US-08-267-803B-81
C 15	11	52.4	30	3	US-08-848-810-42
C 16	10	47.6	16	3	US-09-648-040-8
C 17	10	47.6	16	4	US-09-371-772B-5859
C 18	10	47.6	17	4	US-09-319-265-5
C 19	10	47.6	17	4	US-09-371-772B-4854
C 20	10	47.6	17	4	US-09-371-772B-4855
C 21	10	47.6	18	3	US-09-344-521-22
C 22	10	47.6	19	3	US-09-360-416-81
C 23	10	47.6	20	2	US-08-860-882A-46
C 24	10	47.6	20	3	US-08-875-223-3
C 25	10	47.6	20	3	US-09-011-769A-28
C 26	10	47.6	20	4	US-09-422-978-10903
C 27	10	47.6	20	4	US-09-198-452A-5309

Sequence 5528, Ap  
Sequence 5645, Ap  
Sequence 5646, Ap  
Sequence 11, Appl  
Sequence 19, Appl  
Sequence 22, Appl  
Sequence 7, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 63, Appl  
Sequence 63, Appl  
Sequence 16, Appl  
Sequence 65, Appl  
Sequence 2, Appl  
Sequence 65, Appl  
Sequence 62514, A  
Sequence 4, Appl  
Sequence 7356, Ap

20 4 US-09-198-452A-5528  
20 4 US-09-198-452A-5645  
20 4 US-09-198-452A-5646  
20 4 US-09-922-146-11  
20 4 US-10-023-649A-19  
21 3 US-09-210-896-22  
22 3 US-08-793-044-7  
22 5 PCT-US93-12078-2  
22 5 PCT-US93-12078-3  
23 2 US-08-210-762B-63  
23 3 US-09-106-075A-63  
23 3 US-09-102-831-16  
24 2 US-08-210-762B-65  
24 3 US-09-284-900-2  
24 3 US-09-106-075A-65  
24 4 US-09-270-767-62514  
25 1 US-08-379-926A-4  
25 4 US-09-396-196G-7356

#### ALIGNMENTS

RESULT 1  
US-09-396-196G-18110/c  
; Sequence 18110, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18110  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-18110

Query Match 61.9%; Score 13; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGCGGGA 13  
Db 21 AACCAAGCGGGA 9

RESULT 2  
US-09-396-196G-18111/c  
; Sequence 18111, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18111

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18111

Query Match          61.9%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGA 13
Db 13 AACCAAGAGCGGA 1

RESULT 3
US-09-121-920-26
; Sequence 26, Application US/09121920
; Patent No. 6066460
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Mark W.
; APPLICANT: Kinoshita, No. 6066460iyuki
; TITLE OF INVENTION: METHOD FOR CLONING SECRETED PROTEINS
; FILE REFERENCE: HMV-022.01
; CURRENT APPLICATION NUMBER: US/09/121,920
; CURRENT FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 60/053,586
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: primer
US-09-121-920-26

Query Match          52.4%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAAGAGCGGAG 14
Db 1 CAAGAGCGGAG 11

RESULT 4
US-09-172-045-31
; Sequence 31, Application US/09172045
; Patent No. 6277594
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Nakata, Katsunori
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: Hiraki-03497
; CURRENT APPLICATION NUMBER: US/09/172,045
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: JP98/86979
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP98/121456
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-172-045-31

Query Match          52.4%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAAGAGCGGAG 14
Db 1 CAAGAGCGGAG 11

RESULT 5
US-09-342-325C-31
; Sequence 31, Application US/09342325C
; Patent No. 6500637
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Katsunori, Nakata
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: HIRAKI-03814
; CURRENT APPLICATION NUMBER: US/09/342,325C
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: JP98/86979
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: JP98/121456
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 09/172,045
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-342-325C-31

Query Match          52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAAGAGCGGAG 14
Db 1 CAAGAGCGGAG 11

RESULT 6
US-09-980-052-202/c
; Sequence 202, Application US/099800052
; Patent No. 6670130
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 202
; LENGTH: 20
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; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium porcinum  
 US-09-980-052-202

Query Match 52.4%; Score 11; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGCGGAGCAAC 18  
 |||||  
 Db 20 AGCGGAGCAAC 10

## RESULT 7

US-09-332-522E-81/c  
 ; Sequence 81, Application US/09332522E  
 ; Patent No. 6781028  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Costa, M.  
 ; APPLICANT: Doberstein, S.  
 ; APPLICANT: Elson, S.  
 ; APPLICANT: Ferguson, K.  
 ; APPLICANT: Homberger, S.  
 ; TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND S  
 ; TITLE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METAB  
 ; FILE REFERENCE: 7326-101, EX99-004  
 ; CURRENT APPLICATION NUMBER: US/09/332,522E  
 ; CURRENT FILING DATE: 1999-06-14  
 ; NUMBER OF SEQ ID NOS: 95  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 81  
 ; LENGTH: 22  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide  
 US-09-332-522E-81

Query Match 52.4%; Score 11; DB 4; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGAGCAACGAA 21  
 |||||  
 Db 22 GGAGCAACGAA 12

## RESULT 8

US-09-396-196G-14051  
 ; Sequence 14051, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14051  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-396-196G-14051

Query Match 52.4%; Score 11; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCAAGAGCGGA 13  
 |||||  
 Db 7 CCAAGAGCGGA 17

## RESULT 9

US-09-396-196G-18094/c  
 ; Sequence 18094, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 18094  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-396-196G-18094

Query Match 52.4%; Score 11; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGAGCG 11  
 |||||  
 Db 11 AACCAAGAGCG 1

## RESULT 10

US-09-396-196G-18109/c  
 ; Sequence 18109, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 18109  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-396-196G-18109

Query Match 52.4%; Score 11; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCAAGAGCGGA 13  
 |||||  
 Db 25 CCAAGAGCGGA 15

## RESULT 11

```
US-09-396-196G-66426
; Sequence 66426, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66426

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GAGCGGAGCAA 17
      |||||
Db      14 GAGCGGAGCAA 24

RESULT 12
US-09-396-196G-66427
; Sequence 66427, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66427

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GAGCGGAGCAA 17
      |||||
Db      12 GAGCGGAGCAA 22

RESULT 13
US-09-396-196G-66438
; Sequence 66438, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66438

Query Match      52.4%; Score 11; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCAAGAGCG 11
      |||||
Db      10 GAGCGGAGCAA 20

RESULT 14
US-08-267-803B-81
; Sequence 81, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Ott, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 561415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-267-803B-81

Query Match      52.4%; Score 11; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCAAGAGCG 11
      |||||
Db      10 GAGCGGAGCAA 20
```

Db 19 AACCAAGAGCG 29

## RESULT 15

US-08-848-810-42  
; Sequence 42, Application US/08848810  
; Patent No. 6074851  
; GENERAL INFORMATION:  
; APPLICANT: Deibel Jr., M. R.  
; APPLICANT: Yem, A. W.  
; APPLICANT: Wilson, C. L.  
; TITLE OF INVENTION: Catalytic Macro Molecules Having DCD25B  
; TITLE OF INVENTION: Like Activity  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Company  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/848,810  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wootton, Thomas A.  
; REGISTRATION NUMBER: 35,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-833-7914  
; TELEFAX: 616-833-6897  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-848-810-42

Query Match 52.4%; Score 11; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. NO. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCGGAGCAA 17  
|||||  
Db 4 GAGCGGAGCAA 14

Search completed: September 12, 2005, 18:11:00  
Job time : 60 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 15:58:45 ; Search time 1377.5 Seconds  
(without alignments)  
580.290 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aaccaagagcgagcaacgaa 21

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 42690

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	47.6	25	9 CG712540	CG712540 1119027E0
C 2	10	47.6	28	7 R60473	R60473 yhl3g06.r1
C 3	10	47.6	30	9 AG201067	AG201067 Pan trogl
C 4	9	42.9	19	8 AZ599480	AZ599480 IM0414C20
C 5	9	42.9	20	9 AJ593450	AJ593450 Arabidops
C 6	9	42.9	25	4 BM399181	BM399181 5009-0-54
C 7	9	42.9	28	9 AG203460	AG203460 Pan trogl
C 8	9	42.9	30	8 AZ861916	AZ861916 2M0168K17
C 9	8	38.1	17	9 AJ598448	AJ598448 Arabidops
C 10	8	38.1	18	4 BM398577	BM398577 5009-0-47
C 11	8	38.1	20	1 AU256829	AU256829 AU256829
C 12	8	38.1	20	4 BM397580	BM397580 5009-0-34
C 13	8	38.1	20	4 BM398685	BM398685 5009-0-48
C 14	8	38.1	20	4 BM398964	BM398964 5009-0-51
C 15	8	38.1	20	4 BM398968	BM398968 5009-0-51
C 16	8	38.1	20	8 AZ637794	AZ637794 IM0497D20
C 17	8	38.1	20	8 AZ766411	AZ766411 IM0564B02
C 18	8	38.1	20	8 AZ834769	AZ834769 2M0117F08
C 19	8	38.1	21	4 BM397402	BM397402 5009-0-32
C 20	8	38.1	21	4 BM398994	BM398994 5009-0-51
C 21	8	38.1	21	8 AZ636817	AZ636817 IM0495C20
C 22	8	38.1	21	9 AG190199	AG190199 Pan trogl
C 23	8	38.1	22	1 AI723177	AI723177 fc33f01.x
C 24	8	38.1	22	1 AU257837	AU257837 AU257837

#### ALIGNMENTS

RESULT 1  
CG712540  
LOCUS  
DEFINITION  
CG712540 1119027E01.2EL\_y2 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.  
ACCESSION  
CG712540  
VERSION  
CG712540.1 GI:37738446  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 25)  
REFERENCE  
Walbot,V.  
TITLE  
Maize genomic sequences found using engineered RescueMu transposon  
AUTHORS  
Unpublished (2001)  
JOURNAL  
Contact: Walbot V  
COMMENT  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1119027 row: E column: 01  
Classes: transposon-tagged.  
Location/Qualifiers  
1. .25  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1119 - RescueMu Grid AA"  
/note="Organ: leaf; Vector: RescueMu (engineered from plusScript backbone); Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using

BM398612 5009-0-47  
BM399170 5009-0-54  
AZ326642 1M0049D09  
AZ423444 1M0202J03  
AZ839837 2M0107P11  
BM398108 5009-0-40  
BM398156 5009-0-41  
BM400852 5009-0-8-  
AZ593454 1M0405C03  
AZ822792 2M0096O15  
BM396198 5009-0-18  
BM399525 5009-0-58  
BM399548 5009-0-59  
CF311108 ABF--06-D  
AZ468735 1M0281I14  
AZ491197 1M0324C10  
AZ502375 1M0341F08  
AZ859121 2M0164A07  
AU256438 AU256438  
BM399155 5009-0-54  
BM399247 5009-0-55

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN  
Query Match 47.6%; Score 10; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 AGACGGAGC 15  
Db 11 AGACGGAGC 20

RESULT 2  
R60473/c  
LOCUS  
DEFINITION  
IMAGE:43057 5' similar to SP:SYNP\_RAT P22831 ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
R60473  
R60473.1 GI:831168  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Ruhlberg, T., Soares, M., Tan, P.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE  
JOURNAL  
COMMENT  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilton RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: M13RP1  
High quality sequence stop: 1.  
FEATURES  
source  
1. 28  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:415598"  
/db\_xref="taxon:9606"  
/clone="IMAGE:43057"  
/sex="female"  
/dev\_stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares infant brain INIB"  
/notes="Organ: whole brain; Vector: Lafmid BA; Site 1: Not  
I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
I - oligo(dT) primer [5'  
AAGTGAAGAAATTCGGCGCGAGGAAATTTTTTTTTTTT 3'];  
double-stranded cDNA was ligated to Hind III adaptors  
(Pharmacia), digested with Not I and directionally cloned  
into the Not I and Hind III sites of the Lafmid BA vector.  
Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaído."

ORIGIN  
Query Match 47.6%; Score 10; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 AGCGGAGCAA 17  
Db 24 AGCGGAGCAA 15

RESULT 3  
AG201067/c  
LOCUS  
DEFINITION  
Pan troglodytes DNA, clone: RP43-083G08.TJ, genomic survey  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AG201067  
AG201067.1 GI:45233242  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE  
AUTHORS  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
BAC end sequences of Library RP-43  
Unpublished

TITLE  
JOURNAL  
AUTHORS  
2 (bases 1 to 30)  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
Direct Submission  
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);  
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea  
[E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,  
Tel:82-42-866-7181, Fax:82-42-860-4409]  
Clones are derived from the chimpanzee BAC library RP-43 This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.

COMMENT  
Sequencing: TJ  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.  
Location/Qualifiers  
1. 30  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-083G08.TJ"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES  
source

ORIGIN

Query Match 47.6%; Score 10; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGC 10  
Db 29 AACCAAGAGC 20

RESULT 4  
AZ599480  
LOCUS  
DEFINITION  
1M0414C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0414C20 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AZ599480  
AZ599480.1 GI:11721670  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: C column: 20
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0414C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 42.9%; Score 9; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCGGAGC 15
| | | | | | | |
Db 8 GAGCGGAGC 16

RESULT 5
AJ593450/c
LOCUS
AJ593450
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
380F06, genomic survey sequence.
ACCESSION
AJ593450
VERSION
AJ593450.1 GI:37943074
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: C column: 20
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0414C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 42.9%; Score 9; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCGGAGC 15
| | | | | | | |
Db 8 GAGCGGAGC 16

RESULT 5
AJ593450/c
LOCUS
AJ593450
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
380F06, genomic survey sequence.
ACCESSION
AJ593450
VERSION
AJ593450.1 GI:37943074
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 20)
Balzerque,S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
1..20
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone="J380F06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1..20
/notes="T-DNA flanking sequence
left border"

ORIGIN
Query Match 42.9%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCAACGA 20
| | | | | | | |
Db 10 GAGCAACGA 2

RESULT 6
BM399181
LOCUS
BM399181
DEFINITION
5009-0-54-F03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM399181
VERSION
BM399181.1 GI:18199234
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 25)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
REFERENCE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu

```



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Db          |||||
9 GAGCGGAGC 17

RESULT 9
AJ598448/c
LOCUS      17 bp      DNA      linear      GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
468F11, genomic survey sequence.
ACCESSION  AJ598448
VERSION     1 GI:37948076
KEYWORDS   GSS; right border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE  1
AUTHORS   Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE   22363535
PUBMED    1246565
REFERENCE  2 (bases 1 to 17)
AUTHORS   Balzerque,S.
TITLE     Direct Submission
JOURNAL   Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT   PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).

FEATURES   source
            1..17
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassilewskija"
            /db_xref="taxon:3702"
            /clone="468F11"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            misc_feature 1..17
            /note="T-DNA flanking sequence
            right border"

ORIGIN
Query Match      38.1%; Score 8; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGA 8
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Db 16 AACCAAGA 9

RESULT 10
BM398577
LOCUS      18 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM398577
VERSION     1 GI:18198630
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila

FEATURES   source
            1..20
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="BED0009047"
            /tissue type="brain"
            /clone_lib="3'-directed mouse cDNA library"

ORIGIN
Query Match      38.1%; Score 8; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3
            Location/Qualifiers
                1..18
                /organism="Tetrahymena thermophila"
                /mol_type="mRNA"
                /strain="CU428.1"
                /db_xref="taxon:5911"
                /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                /note="Vector: Bluescript 2 SK+; Details on library
                preparation can be found in Chilcoat and Turkewitz (2001)
                Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGCGGAGC 15
    |||||
Db 4 AGCGGAGC 11

RESULT 11
AU256829/c
LOCUS      20 bp      mRNA      linear      EST 25-APR-2002
DEFINITION AU256829 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0009047 3', mRNA sequence.
ACCESSION  AU256829
VERSION     1 GI:20320851
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            Kato,K. and Matoba,R.
            1 (bases 1 to 20)
            Generation of expressed sequence tags from mouse brain
            Unpublished (2002)
            Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkatoba@nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
            Location/Qualifiers
                1..20
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone="BED0009047"
                /tissue type="brain"
                /clone_lib="3'-directed mouse cDNA library"

ORIGIN
Query Match      38.1%; Score 8; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;

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Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  ACCAAGAG  9
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Db      17  ACCAAGAG 10

RESULT 12
BM397580      20 bp  mRNA      linear      EST 17-JAN-2002
LOCUS      5009-0-34-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION      Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM397580
VERSION      BM397580.1  GI:18197633
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE      1  (bases 1 to 20)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..20
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
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      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      8  AGCGGAGC 15
      |||||
Db      3  AGCGGAGC 10

RESULT 14
BM398964
LOCUS      5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION      Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM398964
VERSION      BM398964.1  GI:18199017
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophores;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE      1  (bases 1 to 20)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..20
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: Bluescript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      8  AGCGGAGC 15
      |||||
Db      2  AGCGGAGC 9

RESULT 13
BM398685
LOCUS      5009-0-48-G09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION      Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM398685
VERSION      BM398685.1  GI:18198738
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE      1  (bases 1 to 20)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago

```

```

920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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      1..20
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      /mol_type="mRNA"
      /strain="CU428.1"
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      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: Bluescript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      8  AGCGGAGC 15
      |||||
Db      3  AGCGGAGC 10

RESULT 14
BM398964
LOCUS      5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION      Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM398964
VERSION      BM398964.1  GI:18199017
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophores;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE      1  (bases 1 to 20)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      Location/Qualifiers
      1..20
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: Bluescript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      8  AGCGGAGC 15
      |||||
Db      2  AGCGGAGC 9

RESULT 15

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BM398968  
LOCUS 20 bp mRNA linear EST 17-JAN-2002  
DEFINITION 5009-0-51-C03.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM398968  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 20)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1..20  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/notes="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
ORIGIN  
Query Match 38.1%; Score 8; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 AGCGGAGC 15  
|||||||  
Db 2 AGCGGAGC 9  
Search completed: September 12, 2005, 18:08:58  
Job time : 1382.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 14:13:38 ; Search time 532.5 Seconds  
(without alignments)  
1910.910 Million cell updates/sec

Title: US-10-721-693-2

Perfect score: 21

Sequence: 1 aattcgtgtcgcgtcttgg 21

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1308090

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	CQ824575
2	21	100.0	21	6	CQ824577
3	19	90.5	21	6	CQ824574
4	19	90.5	21	6	CQ824576
5	12	57.1	22	6	AR568156
6	12	57.1	30	6	AX463675
7	11	52.4	20	6	E30575
8	11	52.4	20	6	AR268863
9	11	52.4	20	6	AR442594
10	11	52.4	30	6	AR098219
11	11	52.4	30	6	BD195066
12	11	52.4	30	6	AR368286
13	10	47.6	17	6	AX736243
14	10	47.6	18	6	AX229718
15	10	47.6	18	6	AX402871
16	10	47.6	18	6	AX822220
17	10	47.6	18	6	AX825860
18	10	47.6	20	6	A32141
19	10	47.6	20	6	A52459

C	20	10	47.6	20	6	AR111715	AR111715 Sequence
C	21	10	47.6	20	6	CQ784255	CQ784255 Sequence
C	22	10	47.6	20	6	AR314772	AR314772 Sequence
C	23	10	47.6	20	6	AR315108	AR315108 Sequence
C	24	10	47.6	20	6	AR315109	AR315109 Sequence
C	25	10	47.6	20	6	AR337038	AR337038 Sequence
C	26	10	47.6	20	6	AX296790	AX296790 Sequence
C	27	10	47.6	20	6	AX537665	AX537665 Sequence
C	28	10	47.6	20	6	AX537695	AX537695 Sequence
C	29	10	47.6	20	6	AX956649	AX956649 Sequence
C	30	10	47.6	20	6	BD128179	BD128179 Primer fo
C	31	10	47.6	21	6	AR164118	AR164118 Sequence
C	32	10	47.6	22	6	A48928	A48928 Sequence 6
C	33	10	47.6	22	6	AR153363	AR153363 Sequence
C	34	10	47.6	22	6	AX801579	AX801579 Sequence
C	35	10	47.6	22	6	AX805811	AX805811 Sequence
C	36	10	47.6	23	6	AR237824	AR237824 Sequence
C	37	10	47.6	24	6	AR526704	AR526704 Sequence
C	38	10	47.6	24	6	AX292157	AX292157 Sequence
C	39	10	47.6	24	6	AX44019	AX44019 Sequence
C	40	10	47.6	24	6	AX445110	AX445110 Sequence
C	41	10	47.6	24	6	AX445735	AX445735 Sequence
C	42	10	47.6	24	6	AX445982	AX445982 Sequence
C	43	10	47.6	25	6	A45566	A45566 Sequence 4
C	44	10	47.6	25	6	A47604	A47604 Sequence 4
C	45	10	47.6	25	6	AR019330	AR019330 Sequence

ALIGNMENTS

RESULT 1	CQ824575	Sequence 2 from Patent WO2004047872.	21 bp	DNA	linear	PAT 21-JUN-2004
LOCUS	CQ824575					
DEFINITION	CQ824575					
ACCESSION	CQ824575					
VERSION	CQ824575.1	GI:49021594				
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS		Kaemmerer, W.F.				
TITLE		Treatment of neurodegenerative disease through intracranial delivery of sirna				
JOURNAL		Patent: WO 2004047872-A 2 10-JUN-2004;				
FEATURES		Medtronic, Inc. (US)				
source		Location/Qualifiers				
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ORIGIN

Query Match	100.0%;	Score 21;	DB 6;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 0.19;		
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AATTCGTTGCTCGCTCTTGG	21	
Db	1	AATTCGTTGCTCGCTCTTGG	21	

RESULT 2

CQ824577	Sequence 4 from Patent WO2004047872.	21 bp	DNA	linear	PAT 21-JUN-2004
LOCUS	CQ824577				
DEFINITION	CQ824577				
ACCESSION	CQ824577				
VERSION	CQ824577.1	GI:49021598			
KEYWORDS					
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			

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REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      1
FEATURES     source
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                /mol_type="unassigned DNA"
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Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 AATCGTTGCTCCGCTCTTGG 21
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Db   1 AATCGTTGCTCCGCTCTTGG 21
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RESULT 3
CQ824574/c
LOCUS      CQ824574      21 bp      DNA      linear      PAT 21-JUN-2004
DEFINITION Sequence 1 from Patent WO2004047872.
ACCESSION  CQ824574
VERSION     CQ824574.1 GI:49021592
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Kaemmerer, W.F.
JOURNAL     Treatment of neurodegenerative disease through intracranial
            delivery of siRNA
FEATURES     source
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              Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
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Query Match      90.5%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 TTCGTTGCTCCGCTCTTGG 21
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Db   21 TTCGTTGCTCCGCTCTTGG 3
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RESULT 4
CQ824576/c
LOCUS      CQ824576      21 bp      DNA      linear      PAT 21-JUN-2004
DEFINITION Sequence 3 from Patent WO2004047872.
ACCESSION  CQ824576
VERSION     CQ824576.1 GI:49021596
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Kaemmerer, W.F.
JOURNAL     Treatment of neurodegenerative disease through intracranial
            delivery of siRNA
            Patent: WO 2004047872-A 3 10-JUN-2004;
FEATURES     source
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Query Match      90.5%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 TTCGTTGCTCCGCTCTTGG 21
    |||||
Db   21 TTCGTTGCTCCGCTCTTGG 3
    |||||

RESULT 6
AX463675
LOCUS      AX463675      30 bp      DNA      linear      PAT 15-JUL-2002
DEFINITION Sequence 13 from Patent WO248185.
ACCESSION  AX463675
VERSION     AX463675.1 GI:21886434
KEYWORDS    Synthetic construct
SOURCE      Synthetic construct
ORGANISM    Synthetic construct
REFERENCE   1 Subtil, A., Parsot, C. and Dautry-Varsat, A.
AUTHORS     Secreted chlamydia polypeptides and method for identifying such
TITLE       polypeptides by their secretion by a type III secretion pathway of
            a gram-negative bacteria
            Patent: WO 0248185-A 13 20-JUN-2002;
            INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
            SCIENTIFIQUE (CNRS) (FR); INSERM (E.P.S.T.) (FR)
JOURNAL
FEATURES     source
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FEATURES     source
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 TTCGTTGCTCCGCTCTTGG 21
    |||||
Db   21 TTCGTTGCTCCGCTCTTGG 3
    |||||

RESULT 5
AR568156
LOCUS      AR568156      22 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 81 from patent US 6781028.
ACCESSION  AR568156
VERSION     AR568156.1 GI:53986443
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Costa, M.R., Doberstein, S.K., Elson, S.L., Ferguson, K.C. and
            Homburger, S.A.
TITLE       Animal models and methods for analysis of lipid metabolism and
            screening of pharmaceutical and pesticidal agents that modulate
            lipid metabolism
            Patent: US 6781028-A 81 24-AUG-2004;
JOURNAL
FEATURES     source
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Query Match      57.1%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 ATTCGTTGCTCC 13
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Db   11 ATTCGTTGCTCC 22
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RESULT 6
AX463675
LOCUS      AX463675      30 bp      DNA      linear      PAT 15-JUL-2002
DEFINITION Sequence 13 from Patent WO248185.
ACCESSION  AX463675
VERSION     AX463675.1 GI:21886434
KEYWORDS    Synthetic construct
SOURCE      Synthetic construct
ORGANISM    Synthetic construct
REFERENCE   1 Subtil, A., Parsot, C. and Dautry-Varsat, A.
AUTHORS     Secreted chlamydia polypeptides and method for identifying such
TITLE       polypeptides by their secretion by a type III secretion pathway of
            a gram-negative bacteria
            Patent: WO 0248185-A 13 20-JUN-2002;
            INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
            SCIENTIFIQUE (CNRS) (FR); INSERM (E.P.S.T.) (FR)
JOURNAL
FEATURES     source
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCGTGTGCTC 12
    |||||
Db 6 AATCGTGTGCTC 17

RESULT 7
E30575/c
LOCUS Neurogenesis-inductive gene. 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Neurogenesis-inductive gene.
ACCESSION E30575
VERSION E30575.1 GI:13017145
KEYWORDS JP 1999341985-A/28.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Katuhiko,M., Jun,A., Kenji,N. and Katunori,N.
TITLE Neurogenesis-inductive Gene
JOURNAL Patent: JP 1999341985-A 28 14-DEC-1999;
COMMENT RIKAGAKU KENKYUSHO
PN JP 1999341985-A/28
PD 14-DEC-1999
PF 30-APR-1998 JP 1998121456
PR KATSUHIKO MIKOSHIBA,JUN ARIGA,KENJI NAGAI,KATSUNORI NAKATA PC
C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K38/00,A61K48/00, PC
C07K14/47,
PC C12N1/21,C12N5/10,C12P21/02/(C12N15/09,C12R1:91), (C12N1/21,
PC C12R1:19),
PC (C12N5/10,C12R1:91), (C12P21/02,C12R1:91), (C12P21/02,C12R1:19),
PC C12N15/00,
PC A61K37/02,A61K37/02,C12N5/00,(C12N15/00,C12R1:91), (C12N5/00,
PC C12R1:91)
CC Strandedness: Single;
CC Topology: Linear;
FT key Location/Qualifiers
FT source 1..20
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Query Match          52.4%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGGCTCTTG 20
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Db 11 CTCGGCTCTTG 1

RESULT 8
AR268863/c
LOCUS Sequence 31 from patent US 6500637. 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 31 from patent US 6500637.
ACCESSION AR268863
VERSION AR268863.1 GI:29699559
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mikoshiba,K., Aruga,J., Nagai,T. and Nakata,K.

TITLE Neurogenesis inducing genes
JOURNAL Patent: US 6500637-A 31 31-DEC-2002;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match          52.4%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGGCTCTTG 20
    |||||
Db 11 CTCGGCTCTTG 1

RESULT 9
AR442594
LOCUS Sequence 202 from patent US 6670130. 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 202 from patent US 6670130.
ACCESSION AR442594
VERSION AR442594.1 GI:42669851
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,C.M., Park,H.K. and Jang,H.J.
TITLE Oligonucleotide for detection and identification of Mycobacteria
JOURNAL Patent: US 6670130-A 202 30-DEC-2003;
FEATURES
source Location/Qualifiers
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Query Match          52.4%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTTGCTCCGCT 16
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Db 10 GTTGCTCCGCT 20

RESULT 10
AR098219/c
LOCUS Sequence 42 from patent US 6074851. 30 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 42 from patent US 6074851.
ACCESSION AR098219
VERSION AR098219.1 GI:12807476
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Deibel,M.R. Jr., Yem,A.W. and Wolfe,C.L.
TITLE Catalytic macro molecules having cdc25B like activity
JOURNAL Patent: US 6074851-A 42 13-JUN-2000;
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match          52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17
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Db 14 TTGCTCCGCTC 4

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RESULT 11
BD195066/c
LOCUS          BD195066          30 bp    DNA          linear          PAT 17-JUL-2003
DEFINITION     Catalytic polymer having CDC25B like activity.
ACCESSION      BD195066
VERSION        BD195066.1 GI:33004824
KEYWORDS       JP 2002515742-A/27.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 30)
AUTHORS        Jr,M.R.D., Yem,A.W. and Wilson,C.L.
TITLE          Catalytic polymer having CDC25B like activity
JOURNAL        Patent: JP 2002515742-A 27 28-MAY-2002;
COMMENT        PHARMACIA & UPJOHN CO
OS            OS Unidentified
PN            PN JP 2002515742-A/27
PD            PD 28-MAY-2002
PF            PF 02-MAY-1997 JP 1997538892
PI            PI 02-MAY-1996 US 60/016748, 07-MAY-1996 US 60/017323
MARTIN R DEIBEL JR,ANTHONY W YEM,CINDY L WILSON PC
C12N15/55,C12N15/54,C12N15/62,C12N9/16,C12N9/10,C12N1/21// PC
(C12N1/21,C12R1:19)
CC            CC Strandedness: Single;
CC            CC Topology: Linear;
CC            CC Catalytic polymer having CDC25B like activity FH Key
LOCATION/Qualifiers
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FEATURES
source
ORIGIN

Query Match          52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCGGCTC 17
    |||||
Db 14 TTGCTCGGCTC 4

RESULT 12
AR368286
LOCUS          AR368286          30 bp    DNA          linear          PAT 12-SEP-2003
DEFINITION     Sequence 6 from patent US 6376240.
ACCESSION      AR368286
VERSION        AR368286.1 GI:34601963
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 30)
AUTHORS        Song,A.M., Chen,Y.-F. and Krensky,A.M.
TITLE          RFLAT-1: a transcription factor that activates RANTES gene
JOURNAL        Patent: US 6376240-A 6 23-APR-2002;
FEATURES       Location/Qualifiers
source        1. .30
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ORIGIN

Query Match          52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCT 11

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1 AATTCGTTGCT 11

Db
RESULT 13
AX736243/c
LOCUS          AX736243          17 bp    DNA          linear          PAT 08-MAY-2003
DEFINITION     Sequence 1833 from Patent WO03025177.
ACCESSION      AX736243
VERSION        AX736243.1 GI:30515520
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Telerman,A., Anson,R. and Tuijnder,M.
TITLE          Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL        Patent: WO 03025177-A 1833 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES       Location/Qualifiers
source        1. .17
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCGCTCTTGG 21
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Db 13 CCGCTCTTGG 4

RESULT 14
AX229718/c
LOCUS          AX229718          18 bp    DNA          linear          PAT 11-SEP-2001
DEFINITION     Sequence 5 from Patent WO0162933.
ACCESSION      AX229718
VERSION        AX229718.1 GI:15591930
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Pantelidis,P.
TITLE          Muteins of interleukin-13 (11-13)
JOURNAL        Patent: WO 0162933-A 5 30-AUG-2001;
              Royal Brompton and Harefield NHS Trust (GB)
FEATURES       Location/Qualifiers
source        1. .18
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ORIGIN

Query Match          47.6%; Score 10; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTCCGCTCT 18
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Db 18 GCTCCGCTCT 9

RESULT 15
AX402871/c
LOCUS          AX402871          18 bp    DNA          linear          PAT 07-JUN-2002

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DEFINITION Sequence 355 from Patent WO0196612.  
ACCESSION AX402871  
VERSION AX402871.1 GI:21387862  
KEYWORDS  
SOURCE Penicillium melinii  
ORGANISM Penicillium melinii  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
REFERENCE 1  
AUTHORS Haugland, R. and Vesper, S.  
TITLE Method of identifying and quantifying specific fungi and bacteria  
JOURNAL Patent: WO 0196612-A 355 20-DEC-2001;  
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
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